

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian-Yuan
Wen, Zilong
Zhong, Zhong
- (ii) TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
- (iii) NUMBER OF SEQUENCES: 25
- (iv) CORRESPONDENCE ADDRESS:
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(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/212,185
(B) FILING DATE: 11-MAR-1994
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/980,498
(B) FILING DATE: 23-NOV-1992
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/854,296
(B) FILING DATE: 19-MAR-1992
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: WO US93/02569
(B) FILING DATE: 19-MAR-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/126,588
(B) FILING DATE: 24-SEP-1993
- (viii) ATTORNEY/AGENT INFORMATION:
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(C) REFERENCE/DOCKET NUMBER: 600-1-073 CIP
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: unknown

0987673.050701
"E29/860"

(ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
 (vii) IMMEDIATE SOURCE:
 (B) CLONE: HeLa
 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 25..2577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACTGCAACCC TAATCAGAGC CCAA ATG GCG CAG TGG GAA ATG CTG CAG AAT	51
Met Ala Gln Trp Glu Met Leu Gln Asn	
1 5	
CTT GAC AGC CCC TTT CAG GAT CAG CTG CAC CAG CTT TAC TCG CAC AGC	99
Leu Asp Ser Pro Phe Gln Asp Gln Leu His Gln Leu Tyr Ser His Ser	
10 15 20 25	
CTC CTG CCT GTG GAC ATT CGA CAG TAC TTG GCT GTC TGG ATT GAA GAC	147
Leu Leu Pro Val Asp Ile Arg Gln Tyr Leu Ala Val Trp Ile Glu Asp	
30 35 40	
CAG AAC TGG CAG GAA GCT GCA CTT GGG AGT GAT GAT TCC AAG GCT ACC	195
Gln Asn Trp Gln Glu Ala Ala Leu Gly Ser Asp Asp Ser Lys Ala Thr	
45 50 55	
ATG CTA TTC TTC CAC TTC TTG GAT CAG CTG AAC TAT GAG TGT GGC CGT	243
Met Leu Phe Phe His Phe Leu Asp Gln Leu Asn Tyr Glu Cys Gly Arg	
60 65 70	
TGC AGC CAG GAC CCA GAG TCC TTG TTG CTG CAG CAC AAT TTG CGG AAA	291
Cys Ser Gln Asp Pro Glu Ser Leu Leu Leu Gln His Asn Leu Arg Lys	
75 80 85	
TTC TGC CGG GAC ATT CAG CCC TTT TCC CAG GAT CCT ACC CAG TTG GCT	339
Phe Cys Arg Asp Ile Gln Pro Phe Ser Gln Asp Pro Thr Gln Leu Ala	
90 95 100 105	
GAG ATG ATC TTT AAC CTC CTT CTG GAA GAA AAA AGA ATT TTG ATC CAG	387
Glu Met Ile Phe Asn Leu Leu Leu Glu Glu Lys Arg Ile Leu Ile Gln	
110 115 120	
GCT CAG AGG GCC CAA TTG GAA CAA GGA GAG CCA GTT CTC GAA ACA CCT	435
Ala Gln Arg Ala Gln Leu Glu Gln Gly Glu Pro Val Leu Glu Thr Pro	
125 130 135	
GTG GAG AGC CAG CAA CAT GAG ATT GAA TCC CGG ATC CTG GAT TTA AGG	483
Val Glu Ser Gln Gln His Glu Ile Glu Ser Arg Ile Leu Asp Leu Arg	
140 145 150	
GCT ATG ATG GAG AAG CTG GTA AAA TCC ATC AGC CAA CTG AAA GAC CAG	531
Ala Met Met Glu Lys Leu Val Lys Ser Ile Ser Gln Leu Lys Asp Gln	
155 160 165	
CAG GAT GTC TTC TGC TTC CGA TAT AAG ATC CAG GCC AAA GGG AAG ACA	579
Gln Asp Val Phe Cys Phe Arg Tyr Lys Ile Gln Ala Lys Gly Lys Thr	
170 175 180 185	

0587573-056701

CCC TCT CTG GAC CCC CAT CAG ACC AAA GAG CAG AAG ATT CTG CAG GAA Pro Ser Leu Asp Pro His Gln Thr Lys Glu Gln Lys Ile Leu Gln Glu 190 195 200	627
ACT CTC AAT GAA CTG GAC AAA AGG AGA AAG GAG GTG CTG GAT GCC TCC Thr Leu Asn Glu Leu Asp Lys Arg Arg Lys Glu Val Leu Asp Ala Ser 205 210 215	675
AAA GCA CTG CTA GGC CGA TTA ACT ACC CTA ATC GAG CTA CTG CTG CCA Lys Ala Leu Leu Gly Arg Leu Thr Thr Leu Ile Glu Leu Leu Leu Pro 220 225 230	723
AAG TTG GAG GAG TGG AAG GCC CAG CAG CAA AAA GCC TGC ATC AGA GCT Lys Leu Glu Glu Trp Lys Ala Gln Gln Gln Lys Ala Cys Ile Arg Ala 235 240 245	771
CCC ATT GAC CAC GGG TTG GAA CAG CTG GAG ACA TGG TTC ACA GCT GGA Pro Ile Asp His Gly Leu Glu Gln Leu Glu Thr Trp Phe Thr Ala Gly 250 255 260 265	819
GCA AAG CTG TTG TTT CAC CTG AGG CAG CTG CTG AAG GAG CTG AAG GGA Ala Lys Leu Leu Phe His Leu Arg Gln Leu Leu Lys Glu Leu Lys Gly 270 275 280	867
CTG AGT TGC CTG GTT AGC TAT CAG GAT GAC CCT CTG ACC AAA GGG GTG Leu Ser Cys Leu Val Ser Tyr Gln Asp Asp Pro Leu Thr Lys Gly Val 285 290 295	915
GAC CTA CGC AAC GCC CAG GTC ACA GAG TTG CTA CAG CGT CTG CTC CAC Asp Leu Arg Asn Ala Gln Val Thr Thr Glu Leu Leu Gln Arg Leu Leu His 300 305 310	963
AGA GCC TTT GTG GTA GAA ACC CAG CCC TGC ATG CCC CAA ACT CCC CAT Arg Ala Phe Val Val Glu Thr Gln Pro Cys Met Pro Gln Thr Pro His 315 320 325	1011
CGA CCC CTC ATC CTC AAG ACT GGC AGC AAG TTC ACC GTC CGA ACA AGG Arg Pro Leu Ile Leu Lys Thr Gly Ser Lys Phe Thr Val Arg Thr Arg 330 335 340 345	1059
CTG CTG GTG AGA CTC CAG GAA GGC AAT GAG TCA CTG ACT GTG GAA GTC Leu Leu Val Arg Leu Gln Glu Gly Asn Glu Ser Leu Thr Val Glu Val 350 355 360	1107
TCC ATT GAC AGG AAT CCT CCT CAA TTA CAA GGC TTC CGG AAG TTC AAC Ser Ile Asp Arg Asn Pro Pro Gln Leu Gln Gly Phe Arg Lys Phe Asn 365 370 375	1155
ATT CTG ACT TCA AAC CAG AAA ACT TTG ACC CCC GAG AAG GGG CAG AGT Ile Leu Thr Ser Asn Gln Lys Thr Leu Thr Pro Glu Lys Gly Gln Ser 380 385 390	1203
CAG GGT TTG ATT TGG GAC TTT GGT TAC CTG ACT CTG GTG GAG CAA CGT Gln Gly Leu Ile Trp Asp Phe Gly Tyr Leu Thr Leu Val Glu Gln Arg 395 400 405	1251
TCA GGT GGT TCA GGA AAG GGC AGC AAT AAG GGG CCA CTA GGT GTG ACA Ser Gly Gly Ser Gly Lys Gly Ser Asn Lys Gly Pro Leu Gly Val Thr 410 415 420 425	1299
GAG GAA CTG CAC ATC ATC AGC TTC ACG GTC AAA TAT ACC TAC CAG GGT Glu Glu Leu His Ile Ile Ser Phe Thr Val Lys Tyr Thr Tyr Gln Gly 430 435 440	1347
CTG AAG CAG GAG CTG AAA ACG GAC ACC CTC CCT GTG GTG ATT ATT TCC Leu Lys Gln Glu Leu Lys Thr Asp Thr Leu Pro Val Val Ile Ile Ser 445 450 455	1395

AAC	ATG	AAC	CAG	CTC	TCA	ATT	GCC	TGG	GCT	TCA	GTT	CTC	TGG	TTC	AAT	1443
Asn	Met	Asn	Gln	Leu	Ser	Ile	Ala	Trp	Ala	Ser	Val	Leu	Trp	Phe	Asn	
		460					465					470				
TTG	CTC	AGC	CCA	AAC	CTT	CAG	AAC	CAG	CAG	TTC	TTC	TCC	AAC	CCC	CCC	1491
Leu	Leu	Ser	Pro	Asn	Leu	Gln	Asn	Gln	Gln	Phe	Phe	Ser	Asn	Pro	Pro	
	475					480					485					
AAG	GCC	CCC	TGG	AGC	TTG	CTG	GGC	CCT	GCT	CTC	AGT	TGG	CAG	TTC	TCC	1539
Lys	Ala	Pro	Trp	Ser	Leu	Leu	Gly	Pro	Ala	Leu	Ser	Trp	Gln	Phe	Ser	
490					495					500					505	
TCC	TAT	GTT	GGC	CGA	GGC	CTC	AAC	TCA	GAC	CAG	CTG	AGC	ATG	CTG	AGA	1587
Ser	Tyr	Val	Gly	Arg	Gly	Leu	Asn	Ser	Asp	Gln	Leu	Ser	Met	Leu	Arg	
			510						515					520		
AAC	AAG	CTG	TTC	GGG	CAG	AAC	TGT	AGG	ACT	GAG	GAT	CCA	TTA	TTG	TCC	1635
Asn	Lys	Leu	Phe	Gly	Gln	Asn	Cys	Arg	Thr	Glu	Asp	Pro	Leu	Leu	Ser	
		525						530					535			
TGG	GCT	GAC	TTC	ACT	AAG	CGA	GAG	AGC	CCT	CCT	GGC	AAG	TTA	CCA	TTC	1683
Trp	Ala	Asp	Phe	Thr	Lys	Arg	Glu	Ser	Pro	Pro	Gly	Lys	Leu	Pro	Phe	
		540					545					550				
TGG	ACA	TGG	CTG	GAC	AAA	ATT	CTG	GAG	TTG	GTA	CAT	GAC	CAC	CTG	AAG	1731
Trp	Thr	Trp	Leu	Asp	Lys	Ile	Leu	Glu	Leu	Val	His	Asp	His	Leu	Lys	
	555					560					565					
GAT	CTC	TGG	AAT	GAT	GGA	CGC	ATC	ATG	GGC	TTT	GTG	AGT	CGG	AGC	CAG	1779
Asp	Leu	Trp	Asn	Asp	Gly	Arg	Ile	Met	Gly	Phe	Val	Ser	Arg	Ser	Gln	
570					575					580					585	
GAG	CGC	CGG	CTG	CTG	AAG	AAG	ACC	ATG	TCT	GGC	ACC	TTT	CTA	CTG	CGC	1827
Glu	Arg	Arg	Leu	Leu	Lys	Lys	Thr	Met	Ser	Gly	Thr	Phe	Leu	Leu	Arg	
			590						595				600			
TTC	AGT	GAA	TCG	TCA	GAA	GGG	GGC	ATT	ACC	TGC	TCC	TGG	GTG	GAG	CAC	1875
Phe	Ser	Glu	Ser	Ser	Glu	Gly	Gly	Ile	Thr	Cys	Ser	Trp	Val	Glu	His	
		605						610					615			
CAG	GAT	GAT	GAC	AAG	GTG	CTC	ATC	TAC	TCT	GTG	CAA	CCG	TAC	ACG	AAG	1923
Gln	Asp	Asp	Asp	Lys	Val	Leu	Ile	Tyr	Ser	Val	Gln	Pro	Tyr	Thr	Lys	
		620					625					630				
GAG	GTG	CTG	CAG	TCA	CTC	CCG	CTG	ACT	GAA	ATC	ATC	CGC	CAT	TAC	CAG	1971
Glu	Val	Leu	Gln	Ser	Leu	Pro	Leu	Thr	Glu	Ile	Ile	Arg	His	Tyr	Gln	
	635					640					645					
TTG	CTC	ACT	GAG	GAG	AAT	ATA	CCT	GAA	AAC	CCA	CTG	CGC	TTC	CTC	TAT	2019
Leu	Leu	Thr	Glu	Glu	Asn	Ile	Pro	Glu	Asn	Pro	Leu	Arg	Phe	Leu	Tyr	
650					655					660					665	
CCC	CGA	ATC	CCC	CGG	GAT	GAA	GCT	TTT	GGG	TGC	TAC	TAC	CAG	GAG	AAA	2067
Pro	Arg	Ile	Pro	Arg	Asp	Glu	Ala	Phe	Gly	Cys	Tyr	Tyr	Gln	Glu	Lys	
			670						675				680			
GTT	AAT	CTC	CAG	GAA	CGG	AGG	AAA	TAC	CTG	AAA	CAC	AGG	CTC	ATT	GTG	2115
Val	Asn	Leu	Gln	Glu	Arg	Arg	Lys	Tyr	Leu	Lys	His	Arg	Leu	Ile	Val	
			685					690					695			
GTC	TCT	AAT	AGA	CAG	GTG	GAT	GAA	CTG	CAA	CAA	CCG	CTG	GAG	CTT	AAG	2163
Val	Ser	Asn	Arg	Gln	Val	Asp	Glu	Leu	Gln	Gln	Pro	Leu	Glu	Leu	Lys	
		700					705					710				
CCA	GAG	CCA	GAG	CTG	GAG	TCA	TTA	GAG	CTG	GAA	CTA	GGG	CTG	GTG	CCA	2211
Pro	Glu	Pro	Glu	Leu	Glu	Ser	Leu	Glu	Leu	Glu	Leu	Gly	Leu	Val	Pro	
	715					720					725					

GAG CCA GAG CTC AGC CTG GAC TTA GAG CCA CTG CTG AAG GCA GGG CTG Glu Pro Glu Leu Ser Leu Asp Leu Glu Pro Leu Leu Lys Ala Gly Leu 730 735 740 745	2259
GAT CTG GGG CCA GAG CTA GAG TCT GTG CTG GAG TCC ACT CTG GAG CCT Asp Leu Gly Pro Glu Leu Glu Ser Val Leu Glu Ser Thr Leu Glu Pro 750 755 760	2307
GTG ATA GAG CCC ACA CTA TGC ATG GTA TCA CAA ACA GTG CCA GAG CCA Val Ile Glu Pro Thr Leu Cys Met Val Ser Gln Thr Val Pro Glu Pro 765 770 775	2355
GAC CAA GGA CCT GTA TCA CAG CCA GTG CCA GAG CCA GAT TTG CCC TGT Asp Gln Gly Pro Val Ser Gln Pro Val Pro Glu Pro Asp Leu Pro Cys 780 785 790	2403
GAT CTG AGA CAT TTG AAC ACT GAG CCA ATG GAA ATC TTC AGA AAC TGT Asp Leu Arg His Leu Asn Thr Glu Pro Met Glu Ile Phe Arg Asn Cys 795 800 805	2451
GTA AAG ATT GAA GAA ATC ATG CCG AAT GGT GAC CCA CTG TTG GCT GGC Val Lys Ile Glu Glu Ile Met Pro Asn Gly Asp Pro Leu Leu Ala Gly 810 815 820 825	2499
CAG AAC ACC GTG GAT GAG GTT TAC GTC TCC CGC CCC AGC CAC TTC TAC Gln Asn Thr Val Asp Glu Val Tyr Val Ser Arg Pro Ser His Phe Tyr 830 835 840	2547
ACT GAT GGA CCC TTG ATG CCT TCT GAC TTC TAGGAACCAC ATTTCTCTCTG Thr Asp Gly Pro Leu Met Pro Ser Asp Phe 845 850	2597
TTCTTTTTCAT ATCTCTTTTGC CCTTCCTACT CCTCATAGCA TGATATTGTT CTCCAAGGAT	2657
GGGAATCAGG CATGTGTCCC TTCCAAGCTG TGTAACTGT TCAAACCTCAG GCCTGTGTGA	2717
CTCCATTGGG GTGAGAGGTG AAAGCATAAC ATGGGTACAG AGGGGACAAC AATGAATCAG	2777
AACAGATGCT GAGCCATAGG TCTAAATAGG ATCCTGGAGG CTGCCTGCTG TGCTGGGAGG	2837
TATAGGGGTC CTGGGGGCAG GCCAGGGCAG TTGACAGGTA CTTGGAGGGC TCAGGGCAGT	2897
GGCTTCTTTC CAGTATGGAA GGATTTCAAC ATTTTAATAG TTGGTTAGGC TAACTGGTG	2957
CATACTGGCA TTGGCCTTGG TGGGGAGCAC AGACACAGGA TAGGACTCCA TTTCTTTCTT	3017
CCATTCTTTC ATGTCTAGGA TAACTTGCTT TCTTCTTTCC TTTACTCCTG GCTCAAGCCC	3077
TGAATTTCTT CTTTTCCTGC AGGGGTTGAG AGCTTTCTGC CTTAGCCTAC CATGTGAAAC	3137
TCTACCCTGA AGAAAGGGAT GGATAGGAAG TAGACCTCTT TTTCTTACCA GTCTCCTCCC	3197
CTACTCTGCC CCCTAAGCTG GCTGTACCTG TTCCTCCCC ATAAAATGAT CCTGCCAATC	3257
TAAAAAAAAA A	3268

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

0987673 060704

Met Ala Gln Trp Glu Met Leu Gln Asn Leu Asp Ser Pro Phe Gln Asp
 1 5 10 15
 Gln Leu His Gln Leu Tyr Ser His Ser Leu Leu Pro Val Asp Ile Arg
 20 25 30
 Gln Tyr Leu Ala Val Trp Ile Glu Asp Gln Asn Trp Gln Glu Ala Ala
 35 40 45
 Leu Gly Ser Asp Asp Ser Lys Ala Thr Met Leu Phe Phe His Phe Leu
 50 55 60
 Asp Gln Leu Asn Tyr Glu Cys Gly Arg Cys Ser Gln Asp Pro Glu Ser
 65 70 75 80
 Leu Leu Leu Gln His Asn Leu Arg Lys Phe Cys Arg Asp Ile Gln Pro
 85 90 95
 Phe Ser Gln Asp Pro Thr Gln Leu Ala Glu Met Ile Phe Asn Leu Leu
 100 105 110
 Leu Glu Glu Lys Arg Ile Leu Ile Gln Ala Gln Arg Ala Gln Leu Glu
 115 120 125
 Gln Gly Glu Pro Val Leu Glu Thr Pro Val Glu Ser Gln Gln His Glu
 130 135 140
 Ile Glu Ser Arg Ile Leu Asp Leu Arg Ala Met Met Glu Lys Leu Val
 145 150 155 160
 Lys Ser Ile Ser Gln Leu Lys Asp Gln Gln Asp Val Phe Cys Phe Arg
 165 170 175
 Tyr Lys Ile Gln Ala Lys Gly Lys Thr Pro Ser Leu Asp Pro His Gln
 180 185 190
 Thr Lys Glu Gln Lys Ile Leu Gln Glu Thr Leu Asn Glu Leu Asp Lys
 195 200 205
 Arg Arg Lys Glu Val Leu Asp Ala Ser Lys Ala Leu Leu Gly Arg Leu
 210 215 220
 Thr Thr Leu Ile Glu Leu Leu Leu Pro Lys Leu Glu Glu Trp Lys Ala
 225 230 235 240
 Gln Gln Gln Lys Ala Cys Ile Arg Ala Pro Ile Asp His Gly Leu Glu
 245 250 255
 Gln Leu Glu Thr Trp Phe Thr Ala Gly Ala Lys Leu Leu Phe His Leu
 260 265 270
 Arg Gln Leu Leu Lys Glu Leu Lys Gly Leu Ser Cys Leu Val Ser Tyr
 275 280 285
 Gln Asp Asp Pro Leu Thr Lys Gly Val Asp Leu Arg Asn Ala Gln Val
 290 295 300
 Thr Glu Leu Leu Gln Arg Leu Leu His Arg Ala Phe Val Val Glu Thr
 305 310 315 320
 Gln Pro Cys Met Pro Gln Thr Pro His Arg Pro Leu Ile Leu Lys Thr
 325 330 335
 Gly Ser Lys Phe Thr Val Arg Thr Arg Leu Leu Val Arg Leu Gln Glu
 340 345 350
 Gly Asn Glu Ser Leu Thr Val Glu Val Ser Ile Asp Arg Asn Pro Pro
 355 360 365

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Gln 370	Leu	Gln	Gly	Phe	Arg	Lys 375	Phe	Asn	Ile	Leu	Thr 380	Ser	Asn	Gln	Lys
Thr 385	Leu	Thr	Pro	Glu	Lys 390	Gly	Gln	Ser	Gln	Gly 395	Leu	Ile	Trp	Asp	Phe 400
Gly	Tyr	Leu	Thr	Leu 405	Val	Glu	Gln	Arg	Ser 410	Gly	Gly	Ser	Gly	Lys 415	Gly
Ser	Asn	Lys	Gly 420	Pro	Leu	Gly	Val	Thr 425	Glu	Glu	Leu	His	Ile 430	Ile	Ser
Phe	Thr	Val 435	Lys	Tyr	Thr	Tyr	Gln 440	Gly	Leu	Lys	Gln	Glu 445	Leu	Lys	Thr
Asp	Thr 450	Leu	Pro	Val	Val	Ile 455	Ile	Ser	Asn	Met	Asn 460	Gln	Leu	Ser	Ile
Ala 465	Trp	Ala	Ser	Val	Leu 470	Trp	Phe	Asn	Leu	Leu 475	Ser	Pro	Asn	Leu	Gln 480
Asn	Gln	Gln	Phe	Phe 485	Ser	Asn	Pro	Pro	Lys 490	Ala	Pro	Trp	Ser	Leu 495	Leu
Gly	Pro	Ala	Leu 500	Ser	Trp	Gln	Phe	Ser 505	Ser	Tyr	Val	Gly	Arg 510	Gly	Leu
Asn	Ser	Asp 515	Gln	Leu	Ser	Met	Leu 520	Arg	Asn	Lys	Leu	Phe 525	Gly	Gln	Asn
Cys	Arg 530	Thr	Glu	Asp	Pro	Leu 535	Leu	Ser	Trp	Ala	Asp 540	Phe	Thr	Lys	Arg
Glu 545	Ser	Pro	Pro	Gly	Lys 550	Leu	Pro	Phe	Trp	Thr 555	Trp	Leu	Asp	Lys	Ile 560
Leu	Glu	Leu	Val	His 565	Asp	His	Leu	Lys	Asp 570	Leu	Trp	Asn	Asp	Gly 575	Arg
Ile	Met	Gly	Phe 580	Val	Ser	Arg	Ser	Gln 585	Glu	Arg	Arg	Leu	Leu 590	Lys	Lys
Thr	Met	Ser 595	Gly	Thr	Phe	Leu	Leu 600	Arg	Phe	Ser	Glu	Ser 605	Ser	Glu	Gly
Gly	Ile 610	Thr	Cys	Ser	Trp	Val 615	Glu	His	Gln	Asp	Asp 620	Asp	Lys	Val	Leu
Ile 625	Tyr	Ser	Val	Gln	Pro 630	Tyr	Thr	Lys	Glu	Val 635	Leu	Gln	Ser	Leu	Pro 640
Leu	Thr	Glu	Ile	Ile 645	Arg	His	Tyr	Gln	Leu 650	Leu	Thr	Glu	Glu	Asn 655	Ile
Pro	Glu	Asn	Pro 660	Leu	Arg	Phe	Leu	Tyr 665	Pro	Arg	Ile	Pro	Arg 670	Asp	Glu
Ala	Phe	Gly 675	Cys	Tyr	Tyr	Gln	Glu 680	Lys	Val	Asn	Leu	Gln 685	Glu	Arg	Arg
Lys	Tyr 690	Leu	Lys	His	Arg	Leu 695	Ile	Val	Val	Ser	Asn 700	Arg	Gln	Val	Asp
Glu 705	Leu	Gln	Gln	Pro	Leu 710	Glu	Leu	Lys	Pro	Glu 715	Pro	Glu	Leu	Glu	Ser 720
Leu	Glu	Leu	Glu	Leu 725	Gly	Leu	Val	Pro	Glu 730	Pro	Glu	Leu	Ser	Leu 735	Asp

Figure 1 consists of 12 line graphs, labeled (a) through (l), each representing a different protein. The y-axis for all graphs is 'Percentage of total protein in the cytosol fraction' ranging from 0 to 100. The x-axis for all graphs is 'Protein'.

- (a) **Actin**: Shows high cytosolic localization across all tissues, generally above 80%.
- (b) **Myosin**: Shows high cytosolic localization, generally above 80%.
- (c) **Myosin II**: Shows high cytosolic localization, generally above 80%.
- (d) **Myosin I**: Shows high cytosolic localization, generally above 80%.
- (e) **Myosin III**: Shows high cytosolic localization, generally above 80%.
- (f) **Myosin IV**: Shows high cytosolic localization, generally above 80%.
- (g) **Myosin V**: Shows high cytosolic localization, generally above 80%.
- (h) **Myosin VI**: Shows high cytosolic localization, generally above 80%.
- (i) **Myosin VII**: Shows high cytosolic localization, generally above 80%.
- (j) **Myosin VIII**: Shows high cytosolic localization, generally above 80%.
- (k) **Myosin IX**: Shows high cytosolic localization, generally above 80%.
- (l) **Myosin X**: Shows high cytosolic localization, generally above 80%.

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3943 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

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(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 197..2449
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ATTAAACCTC	TCGCCGAGCC	CCTCCGCAGA	CTCTGCGCCG	GAAAGTTTCA	TTTGCTGTAT	60										
GCCATCCTCG	AGAGCTGTCT	AGGTAAACGT	TCGCACTCTG	TGTATATAC	CTCGACAGTC	120										
TTGGCACCTA	ACGTGCTGTG	CGTAGCTGCT	CCTTTGGTTG	AATCCCCAGG	CCCTTGTTGG	180										
GGCACAAAGGT	GGCAGG	ATG	TCT	CAG	TGG	TAC	GAA	CTT	CAG	CAG	CTT	GAC	229			
		Met	Ser	Gln	Trp	Tyr	Glu	Leu	Gln	Gln	Leu	Asp				
		1				5					10					
TCA	AAA	TTC	CTG	GAG	CAG	GTT	CAC	CAG	CTT	TAT	GAT	GAC	AGT	TTT	CCC	277
Ser	Lys	Phe	Leu	Glu	Gln	Val	His	Gln	Leu	Tyr	Asp	Asp	Ser	Phe	Pro	
			15					20					25			
ATG	GAA	ATC	AGA	CAG	TAC	CTG	GCA	CAG	TGG	TTA	GAA	AAG	CAA	GAC	TGG	325
Met	Glu	Ile	Arg	Gln	Tyr	Leu	Ala	Gln	Trp	Leu	Glu	Lys	Gln	Asp	Trp	
		30					35					40				

GAG Glu	CAC His 45	GCT Ala	GCC Ala	AAT Asn	GAT Asp	GTT Val 50	TCA Ser	TTT Phe	GCC Ala	ACC Thr	ATC Ile 55	CGT Arg	TTT Phe	CAT His	GAC Asp	373
CTC Leu 60	CTG Leu	TCA Ser	CAG Gln	CTG Leu	GAT Asp 65	GAT Asp	CAA Gln	TAT Tyr	AGT Ser	CGC Arg 70	TTT Phe	TCT Ser	TTG Leu	GAG Glu	AAT Asn 75	421
AAC Asn	TTC Phe	TTG Leu	CTA Leu	CAG Gln 80	CAT His	AAC Asn	ATA Ile	AGG Arg	AAA Lys 85	AGC Ser	AAG Lys	CGT Arg	AAT Asn	CTT Leu 90	CAG Gln	469
GAT Asp	AAT Asn	TTT Phe	CAG Gln 95	GAA Glu	GAC Asp	CCA Pro	ATC Ile	CAG Gln 100	ATG Met	TCT Ser	ATG Met	ATC Ile	ATT Ile 105	TAC Tyr	AGC Ser	517
TGT Cys	CTG Leu	AAG Lys 110	GAA Glu	GAA Glu	AGG Arg	AAA Lys	ATT Ile 115	CTG Leu	GAA Glu	AAC Asn	GCC Ala	CAG Gln 120	AGA Arg	TTT Phe	AAT Asn	565
CAG Gln 125	GCT Ala	CAG Gln	TCG Ser	GGG Gly	AAT Asn	ATT Ile 130	CAG Gln	AGC Ser	ACA Thr	GTG Val	ATG Met 135	TTA Leu	GAC Asp	AAA Lys	CAG Gln	613
AAA Lys 140	GAG Glu	CTT Leu	GAC Asp	AGT Ser	AAA Lys 145	GTC Val	AGA Arg	AAT Asn	GTG Val	AAG Lys 150	GAC Asp	AAG Lys	GTT Val	ATG Met	TGT Cys 155	661
ATA Ile	GAG Glu	CAT His	GAA Glu	ATC Ile 160	AAG Lys	AGC Ser	CTG Leu	GAA Glu	GAT Asp 165	TTA Leu	CAA Gln	GAT Asp	GAA Glu	TAT Tyr 170	GAC Asp	709
TTC Phe	AAA Lys	TGC Cys	AAA Lys 175	ACC Thr	TTG Leu	CAG Gln	AAC Asn	AGA Arg 180	GAA Glu	CAC His	GAG Glu	ACC Thr	AAT Asn 185	GGT Gly	GTG Val	757
GCA Ala	AAG Lys 190	AGT Ser	GAT Asp	CAG Gln	AAA Lys	CAA Gln	GAA Glu 195	CAG Gln	CTG Leu	TTA Leu	CTC Leu	AAG Lys 200	AAG Lys	ATG Met	TAT Tyr	805
TTA Leu 205	ATG Met	CTT Leu	GAC Asp	AAT Asn	AAG Lys	AGA Arg 210	AAG Lys	GAA Glu	GTA Val	GTT Val	CAC His 215	AAA Lys	ATA Ile	ATA Ile	GAG Glu	853
TTG Leu 220	CTG Leu	AAT Asn	GTC Val	ACT Thr	GAA Glu 225	CTT Leu	ACC Thr	CAG Gln	AAT Asn	GCC Ala 230	CTG Leu	ATT Ile	AAT Asn	GAT Asp	GAA Glu 235	901
CTA Leu	GTG Val	GAG Glu	TGG Trp	AAG Lys 240	CGG Arg	AGA Arg	CAG Gln	CAG Gln	AGC Ser 245	GCC Ala	TGT Cys	ATT Ile	GGG Gly	GGG Gly	CCG Pro 250	949
CCC Pro	AAT Asn	GCT Ala	TGC Cys 255	TTG Leu	GAT Asp	CAG Gln	CTG Leu	CAG Gln 260	AAC Asn	TGG Trp	TTC Phe	ACT Thr 265	ATA Ile	GTT Val	GCG Ala	997
GAG Glu	AGT Ser	CTG Leu 270	CAG Gln	CAA Gln	GTT Val	CGG Arg	CAG Gln 275	CAG Gln	CTT Leu	AAA Lys	AAG Lys	TTG Leu 280	GAG Glu	GAA Glu	TTG Leu	1045
GAA Glu 285	CAG Gln	AAA Lys	TAC Tyr	ACC Thr	TAC Tyr	GAA Glu 290	CAT His	GAC Asp	CCT Pro	ATC Ile	ACA Thr 295	AAA Lys	AAC Asn	AAA Lys	CAA Gln	1093
GTG Val 300	TTA Leu	TGG Trp	GAC Asp	CGC Arg	ACC Thr 305	TTC Phe	AGT Ser	CTT Leu	TTC Phe	CAG Gln 310	CAG Gln	CTC Leu	ATT Ile	CAG Gln	AGC Ser 315	1141

TCG	TTT	GTG	GTG	GAA	AGA	CAG	CCC	TGC	ATG	CCA	ACG	CAC	CCT	CAG	AGG	1189
Ser	Phe	Val	Val	Glu	Arg	Gln	Pro	Cys	Met	Pro	Thr	His	Pro	Gln	Arg	
				320					325					330		
CCG	CTG	GTC	TTG	AAG	ACA	GGG	GTC	CAG	TTC	ACT	GTG	AAG	TTG	AGA	CTG	1237
Pro	Leu	Val	Leu	Lys	Thr	Gly	Val	Gln	Phe	Thr	Val	Lys	Leu	Arg	Leu	
				335				340					345			
TTG	GTG	AAA	TTG	CAA	GAG	CTG	AAT	TAT	AAT	TTG	AAA	GTC	AAA	GTC	TTA	1285
Leu	Val	Lys	Leu	Gln	Glu	Leu	Asn	Tyr	Asn	Leu	Lys	Val	Lys	Val	Leu	
		350					355					360				
TTT	GAT	AAA	GAT	GTG	AAT	GAG	AGA	AAT	ACA	GTA	AAA	GGA	TTT	AGG	AAG	1333
Phe	Asp	Lys	Asp	Val	Asn	Glu	Arg	Asn	Thr	Val	Lys	Gly	Phe	Arg	Lys	
	365					370					375					
TTC	AAC	ATT	TTG	GGC	ACG	CAC	ACA	AAA	GTG	ATG	AAC	ATG	GAG	GAG	TCC	1381
Phe	Asn	Ile	Leu	Gly	Thr	His	Thr	Lys	Val	Met	Asn	Met	Glu	Glu	Ser	
	380				385					390					395	
ACC	AAT	GGC	AGT	CTG	GCG	GCT	GAA	TTT	CGG	CAC	CTG	CAA	TTG	AAA	GAA	1429
Thr	Asn	Gly	Ser	Leu	Ala	Ala	Glu	Phe	Arg	His	Leu	Gln	Leu	Lys	Glu	
				400					405					410		
CAG	AAA	AAT	GCT	GGC	ACC	AGA	ACG	AAT	GAG	GGT	CCT	CTC	ATC	GTT	ACT	1477
Gln	Lys	Asn	Ala	Gly	Thr	Arg	Thr	Asn	Glu	Gly	Pro	Leu	Ile	Val	Thr	
			415					420					425			
GAA	GAG	CTT	CAC	TCC	CTT	AGT	TTT	GAA	ACC	CAA	TTG	TGC	CAG	CCT	GGT	1525
Glu	Glu	Leu	His	Ser	Leu	Ser	Phe	Glu	Thr	Gln	Leu	Cys	Gln	Pro	Gly	
		430					435					440				
TTG	GTA	ATT	GAC	CTC	GAG	ACG	ACC	TCT	CTG	CCC	GTT	GTG	GTG	ATC	TCC	1573
Leu	Val	Ile	Asp	Leu	Glu	Thr	Thr	Ser	Leu	Pro	Val	Val	Val	Ile	Ser	
		445				450					455					
AAC	GTC	AGC	CAG	CTC	CCG	AGC	GGT	TGG	GCC	TCC	ATC	CTT	TGG	TAC	AAC	1621
Asn	Val	Ser	Gln	Leu	Pro	Ser	Gly	Trp	Ala	Ser	Ile	Leu	Trp	Tyr	Asn	
	460				465					470					475	
ATG	CTG	GTG	GCG	GAA	CCC	AGG	AAT	CTG	TCC	TTC	TTC	CTG	ACT	CCA	CCA	1669
Met	Leu	Val	Ala	Glu	Pro	Arg	Asn	Leu	Ser	Phe	Phe	Leu	Thr	Pro	Pro	
				480					485					490		
TGT	GCA	CGA	TGG	GCT	CAG	CTT	TCA	GAA	GTG	CTG	AGT	TGG	CAG	TTT	TCT	1717
Cys	Ala	Arg	Trp	Ala	Gln	Leu	Ser	Glu	Val	Leu	Ser	Trp	Gln	Phe	Ser	
			495					500					505			
TCT	GTC	ACC	AAA	AGA	GGT	CTC	AAT	GTG	GAC	CAG	CTG	AAC	ATG	TTG	GGA	1765
Ser	Val	Thr	Lys	Arg	Gly	Leu	Asn	Val	Asp	Gln	Leu	Asn	Met	Leu	Gly	
		510					515					520				
GAG	AAG	CTT	CTT	GGT	CCT	AAC	GCC	AGC	CCC	GAT	GGT	CTC	ATT	CCG	TGG	1813
Glu	Lys	Leu	Leu	Gly	Pro	Asn	Ala	Ser	Pro	Asp	Gly	Leu	Ile	Pro	Trp	
	525					530					535					
ACG	AGG	TTT	TGT	AAG	GAA	AAT	ATA	AAT	GAT	AAA	AAT	TTT	CCC	TTC	TGG	1861
Thr	Arg	Phe	Cys	Lys	Glu	Asn	Ile	Asn	Asp	Lys	Asn	Phe	Pro	Phe	Trp	
	540				545					550					555	
CTT	TGG	ATT	GAA	AGC	ATC	CTA	GAA	CTC	ATT	AAA	AAA	CAC	CTG	CTC	CCT	1909
Leu	Trp	Ile	Glu	Ser	Ile	Leu	Glu	Leu	Ile	Lys	Lys	His	Leu	Leu	Pro	
				560					565					570		
CTC	TGG	AAT	GAT	GGG	TGC	ATC	ATG	GGC	TTC	ATC	AGC	AAG	GAG	CGA	GAG	1957
Leu	Trp	Asn	Asp	Gly	Cys	Ile	Met	Gly	Phe	Ile	Ser	Lys	Glu	Arg	Glu	
			575					580					585			

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CGT GCC CTG TTG AAG GAC CAG CAG CCG GGG ACC TTC CTG CTG CGG TTC Arg Ala Leu Leu Lys Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe 590 595 600	2005
AGT GAG AGC TCC CGG GAA GGG GCC ATC ACA TTC ACA TGG GTG GAG CGG Ser Glu Ser Ser Arg Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg 605 610 615	2053
TCC CAG AAC GGA GGC GAA CCT GAC TTC CAT GCG GTT GAA CCC TAC ACG Ser Gln Asn Gly Gly Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr 620 625 630 635	2101
AAG AAA GAA CTT TCT GCT GTT ACT TTC CCT GAC ATC ATT CGC AAT TAC Lys Lys Glu Leu Ser Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr 640 645 650	2149
AAA GTC ATG GCT GCT GAG AAT ATT CCT GAG AAT CCC CTG AAG TAT CTG Lys Val Met Ala Ala Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu 655 660 665	2197
TAT CCA AAT ATT GAC AAA GAC CAT GCC TTT GGA AAG TAT TAC TCC AGG Tyr Pro Asn Ile Asp Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg 670 675 680	2245
CCA AAG GAA GCA CCA GAG CCA ATG GAA CTT GAT GGC CCT AAA GGA ACT Pro Lys Glu Ala Pro Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr 685 690 695	2293
GGA TAT ATC AAG ACT GAG TTG ATT TCT GTG TCT GAA GTT CAC CCT TCT Gly Tyr Ile Lys Thr Glu Leu Ile Ser Val Ser Glu Val His Pro Ser 700 705 710 715	2341
AGA CTT CAG ACC ACA GAC AAC CTG CTC CCC ATG TCT CCT GAG GAG TTT Arg Leu Gln Thr Thr Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe 720 725 730	2389
GAC GAG GTG TCT CGG ATA GTG GGC TCT GTA GAA TTC GAC AGT ATG ATG Asp Glu Val Ser Arg Ile Val Gly Ser Val Glu Phe Asp Ser Met Met 735 740 745	2437
AAC ACA GTA TAGAGCATGA ATTTTTTTCA TCTTCTCTGG CGACAGTTTT Asn Thr Val 750	2485
CCTTCTCATC TGTGATTCCC TCCTGCTACT CTGTTCTTTC ACATCCTGTG TTTCTAGGGA	2546
AATGAAAGAA AGGCCAGCAA ATTCGCTGCA ACCTGTTGAT AGCAAGTGAA TTTTCTCTA	2606
ACTCAGAAAC ATCAGTTACT CTGAAGGGCA TCATGCATCT TACTGAAGGT AAAATTGAAA	2666
GGCATTCTCT GAAGAGTGGG TTTCACAAGT GAAAAACATC CAGATACACC CAAAGTATCA	2726
GGACGAGAAT GAGGGTCCTT TGGGAAAGGA GAAGTTAAGC AACATCTAGC AAATGTTATG	2786
CATAAAGTCA GTGCCCAACT GTTATAGGTT GTTGGATAAA TCAGTGGTTA TTTAGGGAAC	2846
TGCTTGACGT AGGAACGGTA AATTTCTGTG GGAGAATTCT TACATGTTTT CTTTGCTTTA	2906
AGTGTAAC TGAGTTTTCC ATTGGTTTAC CTGTGAAATA GTTCAAAGCC AAGTTTATAT	2966
ACAATTATAT CAGTCCTCTT TCAAAGGTA CCATCATGGA TCTGGTAGGG GGAAAATGTG	3026
TATTTTATTA CATCTTTTAC ATTGGCTATT TAAAGACAAA GACAAATTCT GTTTCTTGAG	3086
AAGAGAACAT TTCCAAATTC ACAAGTTGTG TTTGATATCC AAAGCTGAAT ACATTCTGCT	3146
TTATCTTTGG TCACATACAA TTATTTTAC AGTTCTCCCA AGGGAGTTAG GCTATTACAA	3206
ACCACTCATT CAAAAGTTGA AATTAACCAT AGATGTAGAT AAACCTCAGAA ATTTAATTCA	3266

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TGTTCCTTAA ATGGGCTACT TTGTCCTTTT TGTTATTAGG GTGGTATTTA GTCTATTAGC 3326
 CACAAAATTG GGAAAGGAGT AGAAAAAGCA GTAAGTGACA ACTTGAATAA TACACCAGAG 3386
 ATAATATGAG AATCAGATCA TTTCAAAACT CATTTCTTAT GTAAGTGCAT TGAGAACTGC 3446
 ATATGTTTCG CTGATATATG TGTTCCTTAC ATTTGCGAAT GGTTCCTTTC TCTCTCCTGT 3506
 ACTTTTTCCTC CTTATCACTG ACACAAAAAG TAGATTAAGA GATGGGTTTG ACAAGGTTCT 3566
 TTTTCCTTTC CTTATCACTG ACACAAAAAG TAGATTAAGA GATGGGTTTG ACAAGGTTCT 3626
 TCCCTTTTAC ATACTGCTGT CTATGTGGCT GTATCTTGTT TTTCCACTAC TGCTACCACA 3686
 ACTATATTAT CATGCAAATG CTGTATTCTT CTTTGGTGGA GATAAAGATT TCTTGAGTTT 3746
 TGTTTTTAAA TTAAAGCTAA AGTATCTGTA TTGCATTAAA TATAATATCG ACACAGTGCT 3806
 TTCCGTGGCA CTGCATACAA TCTGAGGCCT CCTCTCTCAG TTTTATATA GATGGCGAGA 3866
 ACCTAAGTTT CAGTTGATTT TACAATTGAA ATGACTAAAA AACAAAGAAG ACAACATTAA 3926
 AAACAATATT GTTTCTA 3943

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp Ser Lys Phe Leu Glu
 1 5 10 15
 Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg Gln
 20 25 30
 Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala Asn
 35 40 45
 Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln Leu
 50 55 60
 Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu Gln
 65 70 75 80
 His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln Glu
 85 90 95
 Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys Glu Glu
 100 105 110
 Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Ser Gly
 115 120 125
 Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp Ser
 130 135 140
 Lys Val Arg Asn Val Lys Asp Lys Val Met Cys Ile Glu His Glu Ile
 145 150 155 160
 Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys Thr
 165 170 175

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Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp Gln
 180 185 190
 Lys Gln Glu Gln Leu Leu Leu Lys Lys Met Tyr Leu Met Leu Asp Asn
 195 200 205
 Lys Arg Lys Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val Thr
 210 215 220
 Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu Trp Lys
 225 230 235 240
 Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys Leu
 245 250 255
 Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu Gln Gln
 260 265 270
 Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Tyr Thr
 275 280 285
 Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp Asp Arg
 290 295 300
 Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu
 305 310 315 320
 Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys
 325 330 335
 Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys Leu Gln
 340 345 350
 Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys Asp Val
 355 360 365
 Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly
 370 375 380
 Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser Leu
 385 390 395 400
 Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala Gly
 405 410 415
 Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His Ser
 420 425 430
 Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp Leu
 435 440 445
 Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln Leu
 450 455 460
 Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Ala Glu
 465 470 475 480
 Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro Cys Ala Arg Trp Ala
 485 490 495
 Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys Arg
 500 505 510
 Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu Leu Gly
 515 520 525
 Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys
 530 535 540

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Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile Glu Ser
 545 550 555 560
 Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn Asp Gly
 565 570 575
 Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys
 580 585 590
 Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg
 595 600 605
 Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly
 610 615 620
 Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser
 625 630 635 640
 Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala
 645 650 655
 Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp
 660 665 670
 Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro
 675 680 685
 Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr
 690 695 700
 Glu Leu Ile Ser Val Ser Glu Val His Pro Ser Arg Leu Gln Thr Thr
 705 710 715 720
 Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe Asp Glu Val Ser Arg
 725 730 735
 Ile Val Gly Ser Val Glu Phe Asp Ser Met Met Asn Thr Val
 740 745 750

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 197..2335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATTAAACCTC TCGCCGAGCC CCTCCGAGA CTCTGCGCCG GAAAGTTTCA TTTGCTGTAT	60
GCCATCCTCG AGAGCTGTCT AGGTTAACGT TCGCACTCTG TGTATATAAC CTCGACAGTC	120
TTGGCACCTA ACGTGCTGTG CGTAGCTGCT CCTTTGGTTG AATCCCCAGG CCCTTGTTGG	180

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GGCACAAAGGT GGCAGG ATG TCT CAG TGG TAC GAA CTT CAG CAG CTT GAC	229
Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp	
1 5 10	
TCA AAA TTC CTG GAG CAG GTT CAC CAG CTT TAT GAT GAC AGT TTT CCC	277
Ser Lys Phe Leu Glu Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro	
15 20 25	
ATG GAA ATC AGA CAG TAC CTG GCA CAG TGG TTA GAA AAG CAA GAC TGG	325
Met Glu Ile Arg Gln Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp	
30 35 40	
GAG CAC GCT GCC AAT GAT GTT TCA TTT GCC ACC ATC CGT TTT CAT GAC	373
Glu His Ala Ala Asn Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp	
45 50 55	
CTC CTG TCA CAG CTG GAT GAT CAA TAT AGT CGC TTT TCT TTG GAG AAT	421
Leu Leu Ser Gln Leu Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn	
60 65 70 75	
AAC TTC TTG CTA CAG CAT AAC ATA AGG AAA AGC AAG CGT AAT CTT CAG	469
Asn Phe Leu Leu Gln His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln	
80 85 90	
GAT AAT TTT CAG GAA GAC CCA ATC CAG ATG TCT ATG ATC ATT TAC AGC	517
Asp Asn Phe Gln Glu Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser	
95 100 105	
TGT CTG AAG GAA GAA AGG AAA ATT CTG GAA AAC GCC CAG AGA TTT AAT	565
Cys Leu Lys Glu Glu Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn	
110 115 120	
CAG GCT CAG TCG GGG AAT ATT CAG AGC ACA GTG ATG TTA GAC AAA CAG	613
Gln Ala Gln Ser Gly Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln	
125 130 135	
AAA GAG CTT GAC AGT AAA GTC AGA AAT GTG AAG GAC AAG GTT ATG TGT	661
Lys Glu Leu Asp Ser Lys Val Arg Asn Val Lys Asp Lys Val Met Cys	
140 145 150 155	
ATA GAG CAT GAA ATC AAG AGC CTG GAA GAT TTA CAA GAT GAA TAT GAC	709
Ile Glu His Glu Ile Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp	
160 165 170	
TTC AAA TGC AAA ACC TTG CAG AAC AGA GAA CAC GAG ACC AAT GGT GTG	757
Phe Lys Cys Lys Thr Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val	
175 180 185	
GCA AAG AGT GAT CAG AAA CAA GAA CAG CTG TTA CTC AAG AAG ATG TAT	805
Ala Lys Ser Asp Gln Lys Gln Glu Gln Leu Leu Leu Lys Lys Met Tyr	
190 195 200	
TTA ATG CTT GAC AAT AAG AGA AAG GAA GTA GTT CAC AAA ATA ATA GAG	853
Leu Met Leu Asp Asn Lys Arg Lys Glu Val Val His Lys Ile Ile Glu	
205 210 215	
TTG CTG AAT GTC ACT GAA CTT ACC CAG AAT GCC CTG ATT AAT GAT GAA	901
Leu Leu Asn Val Thr Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu	
220 225 230 235	
CTA GTG GAG TGG AAG CGG AGA CAG CAG AGC GCC TGT ATT GGG GGG CCG	949
Leu Val Glu Trp Lys Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro	
240 245 250	
CCC AAT GCT TGC TTG GAT CAG CTG CAG AAC TGG TTC ACT ATA GTT GCG	997
Pro Asn Ala Cys Leu Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala	
255 260 265	
GAG AGT CTG CAG CAA GTT CGG CAG CAG CTT AAA AAG TTG GAG GAA TTG	1045

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Glu Ser Leu Gln Gln Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu	
270 275 280	
GAA CAG AAA TAC ACC TAC GAA CAT GAC CCT ATC ACA AAA AAC AAA CAA	1093
Glu Gln Lys Tyr Thr Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln	
285 290 295	
GTG TTA TGG GAC CGC ACC TTC AGT CTT TTC CAG CAG CTC ATT CAG AGC	1141
Val Leu Trp Asp Arg Thr Phe Ser Leu Phe Gln Leu Ile Gln Ser	
300 305 310 315	
TCG TTT GTG GTG GAA AGA CAG CCC TGC ATG CCA ACG CAC CCT CAG AGG	1189
Ser Phe Val Val Glu Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg	
320 325 330	
CCG CTG GTC TTG AAG ACA GGG GTC CAG TTC ACT GTG AAG TTG AGA CTG	1237
Pro Leu Val Leu Lys Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu	
335 340 345	
TTG GTG AAA TTG CAA GAG CTG AAT TAT AAT TTG AAA GTC AAA GTC TTA	1285
Leu Val Lys Leu Gln Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu	
350 355 360	
TTT GAT AAA GAT GTG AAT GAG AGA AAT ACA GTA AAA GGA TTT AGG AAG	1333
Phe Asp Lys Asp Val Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys	
365 370 375	
TTC AAC ATT TTG GGC ACG CAC ACA AAA GTG ATG AAC ATG GAG GAG TCC	1381
Phe Asn Ile Leu Gly Thr His Thr Lys Val Met Asn Met Glu Glu Ser	
380 385 390 395	
ACC AAT GGC AGT CTG GCG GCT GAA TTT CGG CAC CTG CAA TTG AAA GAA	1429
Thr Asn Gly Ser Leu Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu	
400 405 410	
CAG AAA AAT GCT GGC ACC AGA ACG AAT GAG GGT CCT CTC ATC GTT ACT	1477
Gln Lys Asn Ala Gly Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr	
415 420 425	
GAA GAG CTT CAC TCC CTT AGT TTT GAA ACC CAA TTG TGC CAG CCT GGT	1525
Glu Glu Leu His Ser Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly	
430 435 440	
TTG GTA ATT GAC CTC GAG ACG ACC TCT CTG CCC GTT GTG GTG ATC TCC	1573
Leu Val Ile Asp Leu Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser	
445 450 455	
AAC GTC AGC CAG CTC CCG AGC GGT TGG GCC TCC ATC CTT TGG TAC AAC	1621
Asn Val Ser Gln Leu Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn	
460 465 470 475	
ATG CTG GTG GCG GAA CCC AGG AAT CTG TCC TTC TTC CTG ACT CCA CCA	1669
Met Leu Val Ala Glu Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro	
480 485 490	
TGT GCA CGA TGG GCT CAG CTT TCA GAA GTG CTG AGT TGG CAG TTT TCT	1717
Cys Ala Arg Trp Ala Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser	
495 500 505	
TCT GTC ACC AAA AGA GGT CTC AAT GTG GAC CAG CTG AAC ATG TTG GGA	1765
Ser Val Thr Lys Arg Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly	
510 515 520	
GAG AAG CTT CTT GGT CCT AAC GCC AGC CCC GAT GGT CTC ATT CCG TGG	1813
Glu Lys Leu Leu Gly Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp	
525 530 535	

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ACG AGG TTT TGT AAG GAA AAT ATA AAT GAT AAA AAT TTT CCC TTC TGG	1861
Thr Arg Phe Cys Lys Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp	
540 545 550 555	
CTT TGG ATT GAA AGC ATC CTA GAA CTC ATT AAA AAA CAC CTG CTC CCT	1909
Leu Trp Ile Glu Ser Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro	
560 565 570	
CTC TGG AAT GAT GGG TGC ATC ATG GGC TTC ATC AGC AAG GAG CGA GAG	1957
Leu Trp Asn Asp Gly Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu	
575 580 585	
CGT GCC CTG TTG AAG GAC CAG CAG CCG GGG ACC TTC CTG CTG CGG TTC	2005
Arg Ala Leu Leu Lys Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe	
590 595 600	
AGT GAG AGC TCC CGG GAA GGG GCC ATC ACA TTC ACA TGG GTG GAG CGG	2053
Ser Glu Ser Ser Arg Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg	
605 610 615	
TCC CAG AAC GGA GGC GAA CCT GAC TTC CAT GCG GTT GAA CCC TAC ACG	2101
Ser Gln Asn Gly Gly Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr	
620 625 630 635	
AAG AAA GAA CTT TCT GCT GTT ACT TTC CCT GAC ATC ATT CGC AAT TAC	2149
Lys Lys Glu Leu Ser Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr	
640 645 650	
AAA GTC ATG GCT GCT GAG AAT ATT CCT GAG AAT CCC CTG AAG TAT CTG	2197
Lys Val Met Ala Ala Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu	
655 660 665	
TAT CCA AAT ATT GAC AAA GAC CAT GCC TTT GGA AAG TAT TAC TCC AGG	2245
Tyr Pro Asn Ile Asp Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg	
670 675 680	
CCA AAG GAA GCA CCA GAG CCA ATG GAA CTT GAT GGC CCT AAA GGA ACT	2293
Pro Lys Glu Ala Pro Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr	
685 690 695	
GGA TAT ATC AAG ACT GAG TTG ATT TCT GTG TCT GAA GTG TAAGTGAACA	2342
Gly Tyr Ile Lys Thr Glu Leu Ile Ser Val Ser Glu Val	
700 705 710	
CAGAAGAGTG ACATGTTTAC AAACCTCAAG CCAGCCTTGC TCCTGGCTGG GGCCTGTTGA	2402
AGATGCTTGT ATTTTACTTT TCCATTGTAA TTGCTATCGC CATCACAGCT GAACTTGTTG	2462
AGATCCCCGT GTTACTGCCT ATCAGCATTT TACTACTTTA AAAAAAAAAA AAAAAGCCAA	2522
AAACCAAATT TGTATTTAAG GTATATAAAT TTTCCCAAAA CTGATACCCT TTGAAAAAGT	2582
ATAAATAAAA TGAGCAAAAG TTGAA	2607

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 712 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ser	Gln	Trp	Tyr	Glu	Leu	Gln	Gln	Leu	Asp	Ser	Lys	Phe	Leu	Glu
1				5					10					15	

Gln	Val	His	Gln	Leu	Tyr	Asp	Asp	Ser	Phe	Pro	Met	Glu	Ile	Arg	Gln
			20					25					30		
Tyr	Leu	Ala	Gln	Trp	Leu	Glu	Lys	Gln	Asp	Trp	Glu	His	Ala	Ala	Asn
		35					40					45			
Asp	Val	Ser	Phe	Ala	Thr	Ile	Arg	Phe	His	Asp	Leu	Leu	Ser	Gln	Leu
	50					55					60				
Asp	Asp	Gln	Tyr	Ser	Arg	Phe	Ser	Leu	Glu	Asn	Asn	Phe	Leu	Leu	Gln
	65				70					75					80
His	Asn	Ile	Arg	Lys	Ser	Lys	Arg	Asn	Leu	Gln	Asp	Asn	Phe	Gln	Glu
				85					90					95	
Asp	Pro	Ile	Gln	Met	Ser	Met	Ile	Ile	Tyr	Ser	Cys	Leu	Lys	Glu	Glu
			100					105					110		
Arg	Lys	Ile	Leu	Glu	Asn	Ala	Gln	Arg	Phe	Asn	Gln	Ala	Gln	Ser	Gly
		115					120					125			
Asn	Ile	Gln	Ser	Thr	Val	Met	Leu	Asp	Lys	Gln	Lys	Glu	Leu	Asp	Ser
	130					135					140				
Lys	Val	Arg	Asn	Val	Lys	Asp	Lys	Val	Met	Cys	Ile	Glu	His	Glu	Ile
	145				150					155					160
Lys	Ser	Leu	Glu	Asp	Leu	Gln	Asp	Glu	Tyr	Asp	Phe	Lys	Cys	Lys	Thr
				165					170					175	
Leu	Gln	Asn	Arg	Glu	His	Glu	Thr	Asn	Gly	Val	Ala	Lys	Ser	Asp	Gln
			180					185					190		
Lys	Gln	Glu	Gln	Leu	Leu	Leu	Lys	Lys	Met	Tyr	Leu	Met	Leu	Asp	Asn
		195					200					205			
Lys	Arg	Lys	Glu	Val	Val	His	Lys	Ile	Ile	Glu	Leu	Leu	Asn	Val	Thr
	210					215					220				
Glu	Leu	Thr	Gln	Asn	Ala	Leu	Ile	Asn	Asp	Glu	Leu	Val	Glu	Trp	Lys
				230						235					240
Arg	Arg	Gln	Gln	Ser	Ala	Cys	Ile	Gly	Gly	Pro	Pro	Asn	Ala	Cys	Leu
				245					250					255	
Asp	Gln	Leu	Gln	Asn	Trp	Phe	Thr	Ile	Val	Ala	Glu	Ser	Leu	Gln	Gln
			260					265					270		
Val	Arg	Gln	Gln	Leu	Lys	Lys	Leu	Glu	Glu	Leu	Glu	Gln	Lys	Tyr	Thr
		275					280					285			
Tyr	Glu	His	Asp	Pro	Ile	Thr	Lys	Asn	Lys	Gln	Val	Leu	Trp	Asp	Arg
	290					295					300				
Thr	Phe	Ser	Leu	Phe	Gln	Gln	Leu	Ile	Gln	Ser	Ser	Phe	Val	Val	Glu
	305				310					315					320
Arg	Gln	Pro	Cys	Met	Pro	Thr	His	Pro	Gln	Arg	Pro	Leu	Val	Leu	Lys
				325					330					335	
Thr	Gly	Val	Gln	Phe	Thr	Val	Lys	Leu	Arg	Leu	Leu	Val	Lys	Leu	Gln
			340				345						350		
Glu	Leu	Asn	Tyr	Asn	Leu	L									

(C) STRANDEDNESS: both
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mouse
(vii) IMMEDIATE SOURCE:
 (B) CLONE: Murine Stat91
(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 5..2251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAGG ATG TCA CAG TGG TTC GAG CTT CAG CAG CTG GAC TCC AAG TTC CTG	49
Met Ser Gln Trp Phe Glu Leu Gln Gln Leu Asp Ser Lys Phe Leu	
1 ..5 10 15	
GAG CAG GTC CAC CAG CTG TAC GAT GAC AGT TTC CCC ATG GAA ATC AGA	97
Glu Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg	
20 25 30	
CAG TAC CTG GCC CAG TGG CTG GAA AAG CAA GAC TGG GAG CAC GCT GCC	145
Gln Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala	
35 40 45	
TAT GAT GTC TCG TTT GCG ACC ATC CGC TTC CAT GAC CTC CTC TCA CAG	193
Tyr Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln	
50 55 60	
CTG GAC GAC CAG TAC AGC CGC TTT TCT CTG GAG AAT AAT TTC TTG TTG	241
Leu Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu	
65 70 75	
CAG CAC AAC ATA CGG AAA AGC AAG CGT AAT CTC CAG GAT AAC TTC CAA	289
Gln His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln	
80 85 90 95	
GAA GAT CCC GTA CAG ATG TCC ATG ATC ATC TAC AAC TGT CTG AAG GAA	337
Glu Asp Pro Val Gln Met Ser Met Ile Ile Tyr Asn Cys Leu Lys Glu	
100 105 110	
GAA AGG AAG ATT TTG GAA AAT GCC CAA AGA TTT AAT CAG GCC CAG GAG	385
Glu Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Glu	
115 120 125	
GGA AAT ATT CAG AAC ACT GTG ATG TTA GAT AAA CAG AAG GAG CTG GAC	433
Gly Asn Ile Gln Asn Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp	
130 135 140	
AGT AAA GTC AGA AAT GTG AAG GAT CAA GTC ATG TGC ATA GAG CAG GAA	481
Ser Lys Val Arg Asn Val Lys Asp Gln Val Met Cys Ile Glu Gln Glu	
145 150 155	
ATC AAG ACC CTA GAA GAA TTA CAA GAT GAA TAT GAC TTT AAA TGC AAA	529
Ile Lys Thr Leu Glu Glu Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys	
160 165 170 175	
ACC TCT CAG AAC AGA GAA GGT GAA GCC AAT GGT GTG GCG AAG AGC GAC	577
Thr Ser Gln Asn Arg Glu Gly Glu Ala Asn Gly Val Ala Lys Ser Asp	
180 185 190	

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CAA AAA CAG GAA CAG CTG CTG CTC CAC AAG ATG TTT TTA ATG CTT GAC	625
Gln Lys Gln Glu Gln Leu Leu Leu His Lys Met Phe Leu Met Leu Asp	
195 200 205	
AAT AAG AGA AAG GAG ATA ATT CAC AAA ATC AGA GAG TTG CTG AAT TCC	673
Asn Lys Arg Lys Glu Ile Ile His Lys Ile Arg Glu Leu Leu Asn Ser	
210 215 220	
ATC GAG CTC ACT CAG AAC ACT CTG ATT AAT GAC GAG CTC GTG GAG TGG	721
Ile Glu Leu Thr Gln Asn Thr Leu Ile Asn Asp Glu Leu Val Glu Trp	
225 230 235	
AAG CGA AGG CAG CAG AGC GCC TGC ATC GGG GGA CCG CCC AAC GCC TGC	769
Lys Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys	
240 245 250 255	
CTG GAT CAG CTG CAA ACG TGG TTC ACC ATT GTT GCA GAG ACC CTG CAG	817
Leu Asp Gln Leu Thr Trp Phe Thr Ile Val Ala Glu Thr Leu Gln	
260 265 270	
CAG ATC CGT CAG CAG CTT AAA AAG CTG GAG GAG TTG GAA CAG AAA TTC	865
Gln Ile Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Phe	
275 280 285	
ACC TAT GAG CCC GAC CCT ATT ACA AAA AAC AAG CAG GTG TTG TCA GAT	913
Thr Tyr Glu Pro Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Ser Asp	
290 295 300	
CGA ACC TTC CTC CTC TTC CAG CAG CTC ATT CAG AGC TCC TTC GTG GTA	961
Arg Thr Phe Leu Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val	
305 310 315	
GAA CGA CAG CCG TGC ATG CCC ACT CAC CCG CAG AGG CCC CTG GTC TTG	1009
Glu Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu	
320 325 330 335	
AAG ACT GGG GTA CAG TTC ACT GTC AAG TCG AGA CTG TTG GTG AAA TTG	1057
Lys Thr Gly Val Gln Phe Thr Val Lys Ser Arg Leu Leu Val Lys Leu	
340 345 350	
CAA GAG TCG AAT CTA TTA ACG AAA GTG AAA TGT CAC TTT GAC AAA GAT	1105
Gln Glu Ser Asn Leu Leu Thr Lys Val Lys Cys His Phe Asp Lys Asp	
355 360 365	
GTG AAC GAG AAA AAC ACA GTT AAA GGA TTT CGG AAG TTC AAC ATC TTG	1153
Val Asn Glu Lys Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu	
370 375 380	
GGT ACG CAC ACA AAA GTG ATG AAC ATG GAA GAA TCC ACC AAC GGA AGT	1201
Gly Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser	
385 390 395	
CTG GCA GCT GAG CTC CGA CAC CTG CAA CTG AAG GAA CAG AAA AAC GCT	1249
Leu Ala Ala Glu Leu Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala	
400 405 410 415	
GGG AAC AGA ACT AAT GAG GGG CCT CTC ATT GTC ACC GAA GAA CTT CAC	1297
Gly Asn Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His	
420 425 430	
TCT CTT AGC TTT GAA ACC CAG TTG TGC CAG CCA GGC TTG GTG ATT GAC	1345
Ser Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp	
435 440 445	
CTG GAG ACC ACC TCT CTT CCT GTC GTG GTG ATC TCC AAC GTC AGC CAG	1393
Leu Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln	
450 455 460	

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CTC	CCC	AGT	GGC	TGG	GCG	TCT	ATC	CTG	TGG	TAC	AAC	ATG	CTG	GTG	ACA	1441
Leu	Pro	Ser	Gly	Trp	Ala	Ser	Ile	Leu	Trp	Tyr	Asn	Met	Leu	Val	Thr	
	465					470					475					
GAG	CCC	AGG	AAT	CTC	TCC	TTC	TTC	CTG	AAC	CCC	CCG	TGC	GCG	TGG	TGG	1489
Glu	Pro	Arg	Asn	Leu	Ser	Phe	Phe	Leu	Asn	Pro	Pro	Cys	Ala	Trp	Trp	
	480				485					490					495	
TCC	CAG	CTC	TCA	GAG	GTG	TTG	AGT	TGG	CAG	TTT	TCA	TCA	GTC	ACC	AAG	1537
Ser	Gln	Leu	Ser	Glu	Val	Leu	Ser	Trp	Gln	Phe	Ser	Ser	Val	Thr	Lys	
				500					505					510		
AGA	GGT	CTG	AAC	GCA	GAC	CAG	CTG	AGC	ATG	CTG	GGA	GAG	AAG	CTG	CTG	1585
Arg	Gly	Leu	Asn	Ala	Asp	Gln	Leu	Ser	Met	Leu	Gly	Glu	Lys	Leu	Leu	
			515					520					525			
GGC	CCT	AAT	GCT	GGC	CCT	GAT	GGT	CTT	ATT	CCA	TGG	ACA	AGG	TTT	TGT	1633
Gly	Pro	Asn	Ala	Gly	Pro	Asp	Gly	Leu	Ile	Pro	Trp	Thr	Arg	Phe	Cys	
		530				535						540				
AAG	GAA	AAT	ATT	AAT	GAT	AAA	AAT	TTC	TCC	TTC	TGG	CCT	TGG	ATT	GAC	1681
Lys	Glu	Asn	Ile	Asn	Asp	Lys	Asn	Phe	Ser	Phe	Trp	Pro	Trp	Ile	Asp	
	545					550					555					
ACC	ATC	CTA	GAG	CTC	ATT	AAG	AAC	GAC	CTG	CTG	TGC	CTC	TGG	AAT	GAT	1729
Thr	Ile	Leu	Glu	Leu	Ile	Lys	Asn	Asp	Leu	Leu	Cys	Leu	Trp	Asn	Asp	
	560				565					570					575	
GGG	TGC	ATT	ATG	GGC	TTC	ATC	AGC	AAG	GAG	CGA	GAA	CGC	GCT	CTG	CTC	1777
Gly	Cys	Ile	Met	Gly	Phe	Ile	Ser	Lys	Glu	Arg	Glu	Arg	Ala	Leu	Leu	
				580					585					590		
AAG	GAC	CAG	CAG	CCA	GGG	ACG	TTC	CTG	CTT	AGA	TTC	AGT	GAG	AGC	TCC	1825
Lys	Asp	Gln	Gln	Pro	Gly	Thr	Phe	Leu	Leu	Arg	Phe	Ser	Glu	Ser	Ser	
				595				600					605			
CGG	GAA	GGG	GCC	ATC	ACA	TTC	ACA	TGG	GTG	GAA	CGG	TCC	CAG	AAC	GGA	1873
Arg	Glu	Gly	Ala	Ile	Thr	Phe	Thr	Trp	Val	Glu	Arg	Ser	Gln	Asn	Gly	
		610					615					620				
GGT	GAA	CCT	GAC	TTC	CAT	GCC	GTG	GAG	CCC	TAC	ACG	AAA	AAA	GAA	CTT	1921
Gly	Glu	Pro	Asp	Phe	His	Ala	Val	Glu	Pro	Tyr	Thr	Lys	Lys	Glu	Leu	
	625					630					635					
TCA	GCT	GTT	ACT	TTC	CCA	GAT	ATT	ATT	CGC	AAC	TAC	AAA	GTC	ATG	GCT	1969
Ser	Ala	Val	Thr	Phe	Pro	Asp	Ile	Ile	Arg	Asn	Tyr	Lys	Val	Met	Ala	
	640				645					650					655	
GCC	GAG	AAC	ATA	CCA	GAG	AAT	CCC	CTG	AAG	TAT	CTG	TAC	CCC	AAT	ATT	2017
Ala	Glu	Asn	Ile	Pro	Glu	Asn	Pro	Leu	Lys	Tyr	Leu	Tyr	Pro	Asn	Ile	
				660					665					670		
GAC	AAA	GAC	CAC	GCC	TTT	GGG	AAG	TAT	TAT	TCC	AGA	CCA	AAG	GAA	GCA	2065
Asp	Lys	Asp	His	Ala	Phe	Gly	Lys	Tyr	Tyr	Ser	Arg	Pro	Lys	Glu	Ala	
			675					680					685			
CCA	GAA	CCG	ATG	GAG	CTT	GAC	GAC	CCT	AAG	CGA	ACT	GGA	TAC	ATC	AAG	2113
Pro	Glu	Pro	Met	Glu	Leu	Asp	Asp	Pro	Lys	Arg	Thr	Gly	Tyr	Ile	Lys	
		690					695					700				
ACT	GAG	TTG	ATT	TCT	GTG	TCT	GAA	GTC	CAC	CCT	TCT	AGA	CTT	CAG	ACC	2161
Thr	Glu	Leu	Ile	Ser	Val	Ser	Glu	Val	His	Pro	Ser	Arg	Leu	Gln	Thr	
	705					710					715					
ACA	GAC	AAC	CTG	CTT	CCC	ATG	TCT	CCA	GAG	GAG	TTT	GAT	GAG	ATG	TCC	2209
Thr	Asp	Asn	Leu	Leu	Pro	Met	Ser	Pro	Glu	Glu	Phe	Asp	Glu	Met	Ser	
	720				725					730					735	

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CGG ATA GTG GGC CCC GAA TTT GAC AGT ATG ATG AGC ACA GTA
 Arg Ile Val Gly Pro Glu Phe Asp Ser Met Met Ser Thr Val
 740 745

2251

TAAACACGAA TTTCTCTCTG GCGACA

2277

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Ser	Gln	Trp	Phe	Glu	Leu	Gln	Gln	Leu	Asp	Ser	Lys	Phe	Leu	Glu	1	5	10	15
Gln	Val	His	Gln	Leu	Tyr	Asp	Asp	Ser	Phe	Pro	Met	Glu	Ile	Arg	Gln	20	25	30	
Tyr	Leu	Ala	Gln	Trp	Leu	Glu	Lys	Gln	Asp	Trp	Glu	His	Ala	Ala	Tyr	35	40	45	
Asp	Val	Ser	Phe	Ala	Thr	Ile	Arg	Phe	His	Asp	Leu	Leu	Ser	Gln	Leu	50	55	60	
Asp	Asp	Gln	Tyr	Ser	Arg	Phe	Ser	Leu	Glu	Asn	Asn	Phe	Leu	Leu	Gln	65	70	75	80
His	Asn	Ile	Arg	Lys	Ser	Lys	Arg	Asn	Leu	Gln	Asp	Asn	Phe	Gln	Glu	85	90	95	
Asp	Pro	Val	Gln	Met	Ser	Met	Ile	Ile	Tyr	Asn	Cys	Leu	Lys	Glu	Glu	100	105	110	
Arg	Lys	Ile	Leu	Glu	Asn	Ala	Gln	Arg	Phe	Asn	Gln	Ala	Gln	Glu	Gly	115	120	125	
Asn	Ile	Gln	Asn	Thr	Val	Met	Leu	Asp	Lys	Gln	Lys	Glu	Leu	Asp	Ser	130	135	140	
Lys	Val	Arg	Asn	Val	Lys	Asp	Gln	Val	Met	Cys	Ile	Glu	Gln	Glu	Ile	145	150	155	160
Lys	Thr	Leu	Glu	Glu	Leu	Gln	Asp	Glu	Tyr	Asp	Phe	Lys	Cys	Lys	Thr	165	170	175	
Ser	Gln	Asn	Arg	Glu	Gly	Glu	Ala	Asn	Gly	Val	Ala	Lys	Ser	Asp	Gln	180	185	190	
Lys	Gln	Glu	Gln	Leu	Leu	Leu	His	Lys	Met	Phe	Leu	Met	Leu	Asp	Asn	195	200	205	
Lys	Arg	Lys	Glu	Ile	Ile	His	Lys	Ile	Arg	Glu	Leu	Leu	Asn	Ser	Ile	210	215	220	
Glu	Leu	Thr	Gln	Asn	Thr	Leu	Ile	Asn	Asp	Glu	Leu	Val	Glu	Trp	Lys	225	230	235	240
Arg	Arg	Gln	Gln	Ser	Ala	Cys	Ile	Gly	Gly	Pro	Pro	Asn	Ala	Cys	Leu	245	250	255	
Asp	Gln	Leu	Gln	Thr	Trp	Phe	Thr	Ile	Val	Ala	Glu	Thr	Leu	Gln	Gln	260	265	270	

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Ile	Arg	Gln	Gln	Leu	Lys	Lys	Leu	Glu	Glu	Leu	Glu	Gln	Lys	Phe	Thr		
		275					280					285					
Tyr	Glu	Pro	Asp	Pro	Ile	Thr	Lys	Asn	Lys	Gln	Val	Leu	Ser	Asp	Arg		
		290				295					300						
Thr	Phe	Leu	Leu	Phe	Gln	Gln	Leu	Ile	Gln	Ser	Ser	Phe	Val	Val	Glu		
		305			310					315					320		
Arg	Gln	Pro	Cys	Met	Pro	Thr	His	Pro	Gln	Arg	Pro	Leu	Val	Leu	Lys		
				325					330					335			
Thr	Gly	Val	Gln	Phe	Thr	Val	Lys	Ser	Arg	Leu	Leu	Val	Lys	Leu	Gln		
			340					345					350				
Glu	Ser	Asn	Leu	Leu	Thr	Lys	Val	Lys	Cys	His	Phe	Asp	Lys	Asp	Val		
		355					360					365					
Asn	Glu	Lys	Asn	Thr	Val	Lys	Gly	Phe	Arg	Lys	Phe	Asn	Ile	Leu	Gly		
		370				375					380						
Thr	His	Thr	Lys	Val	Met	Asn	Met	Glu	Glu	Ser	Thr	Asn	Gly	Ser	Leu		
					390					395					400		
Ala	Ala	Glu	Leu	Arg	His	Leu	Gln	Leu	Lys	Glu	Gln	Lys	Asn	Ala	Gly		
				405					410					415			
Asn	Arg	Thr	Asn	Glu	Gly	Pro	Leu	Ile	Val	Thr	Glu	Glu	Leu	His	Ser		
			420					425					430				
Leu	Ser	Phe	Glu	Thr	Gln	Leu	Cys	Gln	Pro	Gly	Leu	Val	Ile	Asp	Leu		
		435					440					445					
Glu	Thr	Thr	Ser	Leu	Pro	Val	Val	Val	Ile	Ser	Asn	Val	Ser	Gln	Leu		
		450				455					460						
Pro	Ser	Gly	Trp	Ala	Ser	Ile	Leu	Trp	Tyr	Asn	Met	Leu	Val	Thr	Glu		
					470					475					480		
Pro	Arg	Asn	Leu	Ser	Phe	Phe	Leu	Asn	Pro	Pro	Cys	Ala	Trp	Trp	Ser		
				485					490					495			
Gln	Leu	Ser	Glu	Val	Leu	Ser	Trp	Gln	Phe	Ser	Ser	Val	Thr	Lys	Arg		
			500					505					510				
Gly	Leu	Asn	Ala	Asp	Gln	Leu	Ser	Met	Leu	Gly	Glu	Lys	Leu	Leu	Gly		
		515					520					525					
Pro	Asn	Ala	Gly	Pro	Asp	Gly	Leu	Ile	Pro	Trp	Thr	Arg	Phe	Cys	Lys		
		530				535					540						
Glu	Asn	Ile	Asn	Asp	Lys	Asn	Phe	Ser	Phe	Trp	Pro	Trp	Ile	Asp	Thr		
		545			550					555				560			
Ile	Leu	Glu	Leu	Ile	Lys	Asn	Asp	Leu	Leu	Cys	Leu	Trp	Asn	Asp	Gly		
				565					570					575			
Cys	Ile	Met	Gly	Phe	Ile	Ser	Lys	Glu	Arg	Glu	Arg	Ala	Leu	Leu	Lys		
			580					585					590				
Asp	Gln	Gln	Pro	Gly	Thr	Phe	Leu	Leu	Arg	Phe	Ser	Glu	Ser	Ser	Arg		
		595					600					605					
Glu	Gly	Ala	Ile	Thr	Phe	Thr	Trp	Val	Glu	Arg	Ser	Gln	Asn	Gly	Gly		
		610				615					620						
Glu	Pro	Asp	Phe	His	Ala	Val	Glu	Pro	Tyr	Thr	Lys	Lys	Glu	Leu	Ser		
		625			630					635				640			

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[illegible]

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(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH:-2375 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: both
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Mouse

(vii) IMMEDIATE SOURCE:
    (A) LIBRARY: splenic/thymic
    (B) CLONE: Murine 13sfl

(ix) FEATURE:
    (A) NAME/KEY: CDS
    (B) LOCATION: 34..2277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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<p>TGCCACTACC TGGACGGAGA GAGAGAGAGC AGC ATG TCT CAG TGG AAT CAA GTC</p> <p>Gln Gln Leu Glu Ile Lys Phe Leu Glu Gln Val Asn Gln Val</p> <p>10 15 20</p>	54
<p>GAC AAC TTT CCT ATG GAA ATC CGG CAT CTG CTA GCT CAG TGG ATT GAG</p> <p>Asp Asn Phe Pro Met Glu Ile Arg His Leu Leu Ala Gln Trp Ile Glu</p> <p>25 30 35</p>	150
<p>ACT CAA GAC TGG GAA GTA GCT TCT AAC AAT GAA ACT ATG GCA ACA ATT</p> <p>Thr Gln Asp Trp Glu Val Ala Ser Asn Asn Glu Thr Met Ala Thr Ile</p> <p>40 45 50 55</p>	198
<p>CTG CTT CAA AAC TTA CTA ATA CAA TTG GAT GAA CAG TTG GGG CGG GTT</p> <p>Leu Leu Gln Asn Leu Leu Ile Gln Leu Asp Glu Gln Leu Gly Arg Val</p> <p>60 65 70</p>	246

TCC	AAA	GAA	AAA	AAT	CTG	CTA	TTG	ATT	CAC	AAT	CTA	AAG	AGA	ATT	AGA	294
Ser	Lys	Glu	Lys	Asn	Leu	Leu	Leu	Ile	His	Asn	Leu	Lys	Arg	Ile	Arg	
			75					80					85			
AAA	GTT	CTT	CAG	GGC	AAG	TTT	CAT	GGA	AAT	CCA	ATG	CAT	GTA	GCT	GTG	342
Lys	Val	Leu	Gln	Gly	Lys	Phe	His	Gly	Asn	Pro	Met	His	Val	Ala	Val	
		90					95					100				
GTA	ATT	TCA	AAT	TGC	TTA	AGG	GAA	GAG	AGG	AGA	ATA	TTG	GCT	GCA	GCC	390
Val	Ile	Ser	Asn	Cys	Leu	Arg	Glu	Glu	Arg	Arg	Ile	Leu	Ala	Ala	Ala	
	105					110					115					
AAC	ATG	CCT	ATC	CAG	GGA	CCT	CTG	GAG	AAA	TCC	TTA	CAG	AGT	TCT	TCA	438
Asn	Met	Pro	Ile	Gln	Gly	Pro	Leu	Glu	Lys	Ser	Leu	Gln	Ser	Ser	Ser	
	120				125					130					135	
GTT	TCT	GAA	AGA	CAA	AGG	AAT	GTG	GAA	CAC	AAA	GTG	TCT	GCC	ATT	AAA	486
Val	Ser	Glu	Arg	Gln	Arg	Asn	Val	Glu	His	Lys	Val	Ser	Ala	Ile	Lys	
				140					145					150		
AAC	AGT	GTG	CAG	ATG	ACA	GAA	CAA	GAT	ACC	AAA	TAC	TTA	GAA	GAC	CTG	534
Asn	Ser	Val	Gln	Met	Thr	Glu	Gln	Asp	Thr	Lys	Tyr	Leu	Glu	Asp	Leu	
			155					160					165			
CAA	GAT	GAG	TTT	GAC	TAC	AGG	TAT	AAA	ACA	ATT	CAG	ACA	ATG	GAT	CAG	582
Gln	Asp	Glu	Phe	Asp	Tyr	Arg	Tyr	Lys	Thr	Ile	Gln	Thr	Met	Asp	Gln	
		170					175					180				
GGT	GAC	AAA	AAC	AGT	ATC	CTG	GTG	AAC	CAG	GAA	GTT	TTG	ACA	CTG	CTG	630
Gly	Asp	Lys	Asn	Ser	Ile	Leu	Val	Asn	Gln	Glu	Val	Leu	Thr	Leu	Leu	
	185					190					195					
CAA	GAA	ATG	CTT	AAT	AGT	CTG	GAC	TTC	AAG	AGA	AAG	GAA	GCA	CTC	AGT	678
Gln	Glu	Met	Leu	Asn	Ser	Leu	Asp	Phe	Lys	Arg	Lys	Glu	Ala	Leu	Ser	
	200				205					210					215	
AAG	ATG	ACG	CAG	ATA	GTG	AAC	GAG	ACA	GAC	CTG	CTC	ATG	AAC	AGC	ATG	726
Lys	Met	Thr	Gln	Ile	Val	Asn	Glu	Thr	Asp	Leu	Leu	Met	Asn	Ser	Met	
				220					225					230		
CTT	CTA	GAA	GAG	CTG	CAG	GAC	TGG	AAA	AAG	CGG	CAC	AGG	ATT	GCC	TGC	774
Leu	Leu	Glu	Gln	Leu	Gln	Asp	Trp	Lys	Lys	Arg	His	Arg	Ile	Ala	Cys	
			235					240					245			
ATT	GGT	GGC	CCG	CTC	CAC	AAT	GGG	CTG	GAC	CAG	CTT	CAG	AAC	TGC	TTT	822
Ile	Gly	Gly	Pro	Leu	His	Asn	Gly	Leu	Asp	Gln	Leu	Gln	Asn	Cys	Phe	
		250					255					260				
ACC	CTA	CTG	GCA	GAG	AGT	CTT	TTC	CAA	CTC	AGA	CAG	CAA	CTG	GAG	AAA	870
Thr	Leu	Leu	Ala	Glu	Ser	Leu	Phe	Gln	Leu	Arg	Gln	Gln	Leu	Glu	Lys	
	265					270					275					
CTA	CAG	GAG	CAA	TCT	ACT	AAA	ATG	ACC	TAT	GAA	GGG	GAT	CCC	ATC	CCT	918
Leu	Gln	Glu	Gln	Ser	Thr	Lys	Met	Thr	Tyr	Glu	Gly	Asp	Pro	Ile	Pro	
	280				285					290					295	
GCT	CAA	AGA	GCA	CAC	CTC	CTG	GAA	AGA	GCT	ACC	TTC	CTG	ATC	TAC	AAC	966
Ala	Gln	Arg	Ala	His	Leu	Leu	Glu	Arg	Ala	Thr	Phe	Leu	Ile	Tyr	Asn	
				300					305					310		
CTT	TTC	AAG	AAC	TCA	TTT	GTG	GTC	GAG	CGA	CAC	GCA	TGC	ATG	CCA	ACG	1014
Leu	Phe	Lys	Asn	Ser	Phe	Val	Val	Glu	Arg	His	Ala	Cys	Met	Pro	Thr	
			315				320						325			
CAC	CCT	CAG	AGG	CCG	ATG	GTA	CTT	AAA	ACC	CTC	ATT	CAG	TTC	ACT	GTA	1062
His	Pro	Gln	Arg	Pro	Met	Val	Leu	Lys	Thr	Leu	Ile	Gln	Phe	Thr	Val	
		330					335					340				

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AAA Lys	CTG Leu	AGA Arg	TTA Leu	CTA Leu	ATA Ile	AAA Lys	TTG Leu	CCG Pro	GAA Glu	CTA Leu	AAC Asn	TAT Tyr	CAG Gln	GTG Val	AAA Lys	1110
345						350					355					
GTA Val	AAG Lys	GCG Ala	TCC Ser	ATT Ile	GAC Asp	AAG Lys	AAT Asn	GTT Val	TCA Ser	ACT Thr	CTA Leu	AGC Ser	AAT Asn	AGA Arg	AGA Arg	1158
360					365					370					375	
TTT Phe	GTG Val	CTT Leu	TGT Cys	GGA Gly	ACT Thr	CAC His	GTC Val	AAA Lys	GCT Ala	ATG Met	TCC Ser	AGT Ser	GAG Glu	GAA Glu	TCT Ser	1206
				380					385					390		
TCC Ser	AAT Asn	GGG Gly	AGC Ser	CTC Leu	TCA Ser	GTG Val	GAG Glu	TTA Leu	GAC Asp	ATT Ile	GCA Ala	ACC Thr	CAA Gln	GGA Gly	GAT Asp	1254
			395					400					405			
GAA Glu	GTG Val	CAG Gln	TAC Tyr	TGG Trp	AGT Ser	AAA Lys	GGA Gly	AAC Asn	GAG Glu	GGC Gly	TGC Cys	CAC His	ATG Met	GTG Val	ACA Thr	1302
		410					415					420				
GAG Glu	GAG Glu	TTG Leu	CAT His	TCC Ser	ATA Ile	ACC Thr	TTT Phe	GAG Glu	ACC Thr	CAG Gln	ATC Ile	TGC Cys	CTC Leu	TAT Tyr	GGC Gly	1350
	425					430					435					
CTC Leu	ACC Thr	ATT Ile	AAC Asn	CTA Leu	GAG Glu	ACC Thr	AGC Ser	TCA Ser	TTA Leu	CCT Pro	GTC Val	GTG Val	ATG Met	ATT Ile	TCT Ser	1398
440					445					450					455	
AAT Asn	GTC Val	AGC Ser	CAA Gln	CTA Leu	CCT Pro	AAT Asn	GCA Ala	TGG Trp	GCA Ala	TCC Ser	ATC Ile	ATT Ile	TGG Trp	TAC Tyr	AAT Asn	1446
				460					465					470		
GTA Val	TCA Ser	ACT Thr	AAC Asn	GAC Asp	TCC Ser	CAG Gln	AAC Asn	TTG Leu	GTT Val	TTC Phe	TTT Phe	AAT Asn	AAC Asn	CCT Pro	CCA Pro	1494
			475					480					485			
TCT Ser	GTC Val	ACT Thr	TTG Leu	GGC Gly	CAA Gln	CTC Leu	CTG Leu	GAA Glu	GTG Val	ATG Met	AGC Ser	TGG Trp	CAA Gln	TTT Phe	TCA Ser	1542
		490					495					500				
TCC Ser	TAT Tyr	GTC Val	GGT Gly	CGT Arg	GGC Gly	CTT Leu	AAT Asn	TCA Ser	GAG Glu	CAG Gln	CTC Leu	AAC Asn	ATG Met	CTG Leu	GCA Ala	1590
	505					510					515					
GAG Glu	AAG Lys	CTC Leu	ACA Thr	GTT Val	CAG Gln	TCT Ser	AAC Asn	TAC Tyr	AAT Asn	GAT Asp	GGT Gly	CAC His	CTC Leu	ACC Thr	TGG Trp	1638
520					525					530					535	
GCC Ala	AAG Lys	TTC Phe	TGC Cys	AAG Lys	GAA Glu	CAT His	TTG Leu	CCT Pro	GGC Gly	AAA Lys	ACA Thr	TTT Phe	ACC Thr	TTC Phe	TGG Trp	1686
				540					545					550		
ACT Thr	TGG Trp	CTT Leu	GAA Glu	GCA Ala	ATA Ile	TTG Leu	GAC Asp	CTA Leu	ATT Ile	AAA Lys	AAA Lys	CAT His	ATT Ile	CTT Leu	CCC Pro	1734
			555					560					565			
CTC Leu	TGG Trp	ATT Ile	GAT Asp	GGG Gly	TAC Tyr	ATC Ile	ATG Met	GGA Gly	TTT Phe	GTT Val	AGT Ser	AAA Lys	GAG Glu	AAG Lys	GAA Glu	1782
		570					575					580				
CGG Arg	CTT Leu	CTG Leu	CTC Leu	AAA Lys	GAT Asp	AAA Lys	ATG Met	CCT Pro	GGG Gly	ACA Thr	TTT Phe	TTG Leu	TTA Leu	AGA Arg	TTC Phe	1

[illegible]

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ser	Gln	Trp	Asn	Gln	Val	Gln	Gln	Leu	Glu	Ile	Lys	Phe	Leu	Glu
1				5					10					15	
Gln	Val	Asp	Gln	Phe	Tyr	Asp	Asp	Asn	Phe	Pro	Met	Glu	Ile	Arg	His
			20					25					30		
Leu	Leu	Ala	Gln	Trp	Ile	Glu	Thr	Gln	Asp	Trp	Glu	Val	Ala	Ser	Asn
		35					40					45			
Asn	Glu	Thr	Met	Ala	Thr	Ile	Leu	Leu	Gln	Asn	Leu	Leu	Ile	Gln	Leu
	50					55					60				
Asp	Glu	Gln	Leu	Gly	Arg	Val	Ser	Lys	Glu	Lys	Asn	Leu	Leu	Leu	Ile
65					70					75					80
His	Asn	Leu	Lys	Arg	Ile	Arg	Lys	Val	Leu	Gln	Gly	Lys	Phe	His	Gly
				85					90					95	

Asn	Pro	Met	His	Val	Ala	Val	Val	Ile	Ser	Asn	Cys	Leu	Arg	Glu	Glu	100	105	110
Arg	Arg	Ile	Leu	Ala	Ala	Ala	Asn	Met	Pro	Ile	Gln	Gly	Pro	Leu	Glu	115	120	125
Lys	Ser	Leu	Gln	Ser	Ser	Ser	Val	Ser	Glu	Arg	Gln	Arg	Asn	Val	Glu	130	135	140
His	Lys	Val	Ser	Ala	Ile	Lys	Asn	Ser	Val	Gln	Met	Thr	Glu	Gln	Asp	145	150	155
Thr	Lys	Tyr	Leu	Glu	Asp	Leu	Gln	Asp	Glu	Phe	Asp	Tyr	Arg	Tyr	Lys	165	170	175
Thr	Ile	Gln	Thr	Met	Asp	Gln	Gly	Asp	Lys	Asn	Ser	Ile	Leu	Val	Asn	180	185	190
Gln	Glu	Val	Leu	Thr	Leu	Leu	Gln	Glu	Met	Leu	Asn	Ser	Leu	Asp	Phe	195	200	205
Lys	Arg	Lys	Glu	Ala	Leu	Ser	Lys	Met	Thr	Gln	Ile	Val	Asn	Glu	Thr	210	215	220
Asp	Leu	Leu	Met	Asn	Ser	Met	Leu	Leu	Glu	Glu	Leu	Gln	Asp	Trp	Lys	225	230	235
Lys	Arg	His	Arg	Ile	Ala	Cys	Ile	Gly	Gly	Pro	Leu	His	Asn	Gly	Leu	245	250	255
Asp	Gln	Leu	Gln	Asn	Cys	Phe	Thr	Leu	Leu	Ala	Glu	Ser	Leu	Phe	Gln	260	265	270
Leu	Arg	Gln	Gln	Leu	Glu	Lys	Leu	Gln	Glu	Gln	Ser	Thr	Lys	Met	Thr	275	280	285
Tyr	Glu	Gly	Asp	Pro	Ile	Pro	Ala	Gln	Arg	Ala	His	Leu	Leu	Glu	Arg	290	295	300
Ala	Thr	Phe	Leu	Ile	Tyr	Asn	Leu	Phe	Lys	Asn	Ser	Phe	Val	Val	Glu	305	310	315
Arg	His	Ala	Cys	Met	Pro	Thr	His	Pro	Gln	Arg	Pro	Met	Val	Leu	Lys	325	330	335
Thr	Leu	Ile	Gln	Phe	Thr	Val	Lys	Leu	Arg	Leu	Leu	Ile	Lys	Leu	Pro	340	345	350
Glu	Leu	Asn	Tyr	Gln	Val	Lys	Val	Lys	Ala	Ser	Ile	Asp	Lys	Asn	Val	355	360	365
Ser	Thr	Leu	Ser	Asn	Arg	Arg	Phe	Val	Leu	Cys	Gly	Thr	His	Val	Lys	370	375	380
Ala	Met	Ser	Ser	Glu	Glu	Ser	Ser	Asn	Gly	Ser	Leu	Ser	Val	Glu	Leu	385	390	395
Asp	Ile	Ala	Thr	Gln	Gly	Asp	Glu	Val	Gln	Tyr	Trp	Ser	Lys	Gly	Asn	405	410	415
Glu	Gly	Cys	His	Met	Val	Thr	Glu	Glu	Leu	His	Ser	Ile	Thr	Phe	Glu	420	425	430
Thr	Gln	Ile	Cys	Leu	Tyr	Gly	Leu	Thr	Ile	Asn	Leu	Glu	Thr	Ser	Ser	435	440	445
Leu	Pro	Val	Val	Met	Ile	Ser	Asn	Val	Ser	Gln	Leu	Pro	Asn	Ala	Trp	450	455	460

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Ala Ser Ile Ile Trp Tyr Asn Val Ser Thr Asn Asp Ser Gln Asn Leu
 465 470 475 480
 Val Phe Phe Asn Asn Pro Pro Ser Val Thr Leu Gly Gln Leu Leu Glu
 485 490 495
 Val Met Ser Trp Gln Phe Ser Ser Tyr Val Gly Arg Gly Leu Asn Ser
 500 505 510
 Glu Gln Leu Asn Met Leu Ala Glu Lys Leu Thr Val Gln Ser Asn Tyr
 515 520 525
 Asn Asp Gly His Leu Thr Trp Ala Lys Phe Cys Lys Glu His Leu Pro
 530 535 540
 Gly Lys Thr Phe Thr Phe Trp Thr Trp Leu Glu Ala Ile Leu Asp Leu
 545 550 555 560
 Ile Lys Lys His Ile Leu Pro Leu Trp Ile Asp Gly Tyr Ile Met Gly
 565 570 575
 Phe Val Ser Lys Glu Lys Glu Arg Leu Leu Leu Lys Asp Lys Met Pro
 580 585 590
 Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser His Leu Gly Gly Ile Thr
 595 600 605
 Phe Thr Trp Val Asp Gln Ser Glu Asn Gly Glu Val Arg Phe His Ser
 610 615 620
 Val Glu Pro Tyr Asn Lys Gly Arg Leu Ser Ala Leu Ala Phe Ala Asp
 625 630 635 640
 Ile Leu Arg Asp Tyr Lys Val Ile Met Ala Glu Asn Ile Pro Glu Asn
 645 650 655
 Pro Leu Lys Tyr Leu Tyr Pro Asp Ile Pro Lys Asp Lys Ala Phe Gly
 660 665 670
 Lys His Tyr Ser Ser Gln Pro Cys Glu Val Ser Arg Pro Thr Glu Arg
 675 680 685
 Gly Asp Lys Gly Tyr Val Pro Ser Val Phe Ile Pro Ile Ser Thr Ile
 690 695 700
 Arg Ser Asp Ser Thr Glu Pro Gln Ser Pro Ser Asp Leu Leu Pro Met
 705 710 715 720
 Ser Pro Ser Ala Tyr Ala Val Leu Arg Glu Asn Leu Ser Pro Thr Thr
 725 730 735
 Ile Glu Thr Ala Met Asn Ser Pro Tyr Ser Ala Glu
 740 745

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2869 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

09876773-060704

(A) ORGANISM: Mouse

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: splenic/thymic

(B) CLONE: Murine 19sf6

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 69..2378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCCGCGACCA GCCAGGCCGG CCAGTCGGGC TCAGCCCGGA GACAGTCGAG ACCCCTGACT	60
GCAGCAGG ATG GCT CAG TGG AAC CAG CTG CAG CAG CTG GAC ACA CGC TAC	110
Met Ala Gln Trp Asn Gln Leu Gln Gln Leu Asp Thr Arg Tyr	
1 5 10	
CTG AAG CAG CTG CAC CAG CTG TAC AGC GAC ACG TTC CCC ATG GAG CTG	158
Leu Lys Gln Leu His Gln Leu Tyr Ser Asp Thr Phe Pro Met Glu Leu	
15 20 25 30	
CGG CAG TTC CTG GCA CCT TGG ATT GAG AGT CAA GAC TGG GCA TAT GCA	206
Arg Gln Phe Leu Ala Pro Trp Ile Glu Ser Gln Asp Trp Ala Tyr Ala	
35 40 45	
GCC AGC AAA GAG TCA CAT GCC ACG TTG GTG TTT CAT AAT CTC TTG GGT	254
Ala Ser Lys Glu Ser His Ala Thr Leu Val Phe His Asn Leu Leu Gly	
50 55 60	
GAA ATT GAC CAG CAA TAT AGC CGA TTC CTG CAA GAG TCC AAT GTC CTC	302
Glu Ile Asp Gln Gln Tyr Ser Arg Phe Leu Gln Glu Ser Asn Val Leu	
65 70 75	
TAT CAG CAC AAC CTT CGA AGA ATC AAG CAG TTT CTG CAG AGC AGG TAT	350
Tyr Gln His Asn Leu Arg Arg Ile Lys Gln Phe Leu Gln Ser Arg Tyr	
80 85 90	
CTT GAG AAG CCA ATG GAA ATT GCC CGG ATC GTG GCC CGA TGC CTG TGG	398
Leu Glu Lys Pro Met Glu Ile Ala Arg Ile Val Ala Arg Cys Leu Trp	
95 100 105 110	
GAA GAG TCT CGC CTC CTC CAG ACG GCA GCC ACG GCA GCC CAG CAA GGG	446
Glu Glu Ser Arg Leu Leu Gln Thr Ala Ala Thr Ala Ala Gln Gln Gly	
115 120 125	
GGC CAG GCC AAC CAC CCA ACA GCC GCC GTA GTG ACA GAG AAG CAG CAG	494
Gly Gln Ala Asn His Pro Thr Ala Ala Val Val Thr Glu Lys Gln Gln	
130 135 140	
ATG TTG GAG CAG CAT CTT CAG GAT GTC CGG AAG CGA GTG CAG GAT CTA	542
Met Leu Glu Gln His Leu Gln Asp Val Arg Lys Arg Val Gln Asp Leu	
145 150 155	
GAA CAG AAA ATG AAG GTG GTG GAG AAC CTC CAG GAC GAC TTT GAT TTC	590
Glu Gln Lys Met Lys Val Val Glu Asn Leu Gln Asp Asp Phe Asp Phe	
160 165 170	
AAC TAC AAA ACC CTC AAG AGC CAA GGA GAC ATG CAG GAT CTG AAT GGA	638
Asn Tyr Lys Thr Leu Lys Ser Gln Gly Asp Met Gln Asp Leu Asn Gly	
175 180 185 190	
AAC AAC CAG TCT GTG ACC AGA CAG AAG ATG CAG CAG CTG GAA CAG ATG	686
Asn Asn Gln Ser Val Thr Arg Gln Lys Met Gln Gln Leu Glu Gln Met	
195 200 205	

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CTC	ACA	GCC	CTG	GAC	CAG	ATG	CGG	AGA	AGC	ATT	GTG	AGT	GAG	CTG	GCG	734
Leu	Thr	Ala	Leu	Asp	Gln	Met	Arg	Arg	Ser	Ile	Val	Ser	Glu	Leu	Ala	
			210					215					220			
GGG	CTC	TTG	TCA	GCA	ATG	GAG	TAC	GTG	CAG	AAG	ACA	CTG	ACT	GAT	GAA	782
Gly	Leu	Leu	Ser	Ala	Met	Glu	Tyr	Val	Gln	Lys	Thr	Leu	Thr	Asp	Glu	
		225					230					235				
GAG	CTG	GCT	GAC	TGG	AAG	AGG	CGG	CCA	GAG	ATC	GCG	TGC	ATC	GGA	GGC	830
Glu	Leu	Ala	Asp	Trp	Lys	Arg	Arg	Pro	Glu	Ile	Ala	Cys	Ile	Gly	Gly	
	240					245					250					
CCT	CCC	AAC	ATC	TGC	CTG	GAC	CGT	CTG	GAA	AAC	TGG	ATA	ACT	TCA	TTA	878
Pro	Pro	Asn	Ile	Cys	Leu	Asp	Arg	Leu	Glu	Asn	Trp	Ile	Thr	Ser	Leu	
255					260					265					270	
GCA	GAA	TCT	CAA	CTT	CAG	ACC	CGC	CAA	CAA	ATT	AAG	AAA	CTG	GAG	GAG	926
Ala	Glu	Ser	Gln	Leu	Gln	Thr	Arg	Gln	Gln	Ile	Lys	Lys	Leu	Glu	Glu	
				275						280				285		
CTG	CAG	CAG	AAA	GTG	TCC	TAC	AAG	GGC	GAC	CCT	ATC	GTG	CAG	CAC	CGG	974
Leu	Gln	Gln	Lys	Val	Ser	Tyr	Lys	Gly	Asp	Pro	Ile	Val	Gln	His	Arg	
			290					295					300			
CCC	ATG	CTG	GAG	GAG	AGG	ATC	GTG	GAG	CTG	TTC	AGA	AAC	TTA	ATG	AAG	1022
Pro	Met	Leu	Glu	Glu	Arg	Ile	Val	Glu	Leu	Phe	Arg	Asn	Leu	Met	Lys	
		305					310					315				
AGT	GCC	TTC	GTG	GTG	GAG	CGG	CAG	CCC	TGC	ATG	CCC	ATG	CAC	CCG	GAC	1070
Ser	Ala	Phe	Val	Val	Glu	Arg	Gln	Pro	Cys	Met	Pro	Met	His	Pro	Asp	
	320					325					330					
CGG	CCC	TTA	GTC	ATC	AAG	ACT	GGT	GTC	CAG	TTT	ACC	ACG	AAA	GTC	AGG	1118
Arg	Pro	Leu	Val	Ile	Lys	Thr	Gly	Val	Gln	Phe	Thr	Thr	Lys	Val	Arg	
335					340					345				350		
TTG	CTG	GTC	AAA	TTT	CCT	GAG	TTG	AAT	TAT	CAG	CTT	AAA	ATT	AAA	GTG	1166
Leu	Leu	Val	Lys	Phe	Pro	Glu	Leu	Asn	Tyr	Gln	Leu	Lys	Ile	Lys	Val	
				355					360					365		
TGC	ATT	GAT	AAA	GAC	TCT	GGG	GAT	GTT	GCT	GCC	CTC	AGA	GGG	TCT	CGG	1214
Cys	Ile	Asp	Lys	Asp	Ser	Gly	Asp	Val	Ala	Ala	Leu	Arg	Gly	Ser	Arg	
			370				375						380			
AAA	TTT	AAC	ATT	CTG	GGC	ACG	AAC	ACA	AAA	GTG	ATG	AAC	ATG	GAG	GAG	1262
Lys	Phe	Asn	Ile	Leu	Gly	Thr	Asn	Thr	Lys	Val	Met	Asn	Met	Glu	Glu	
		385					390				395					
TCT	AAC	AAC	GGC	AGC	CTG	TCT	GCA	GAG	TTC	AAG	CAC	CTG	ACC	CTT	AGG	1310
Ser	Asn	Asn	Gly	Ser	Leu	Ser	Ala	Glu	Phe	Lys	His	Leu	Thr	Leu	Arg	
	400					405					410					
GAG	CAG	AGA	TGT	GGG	AAT	GGA	GGC	CGT	GCC	AAT	TGT	GAT	GCC	TCC	TTG	1353
Glu	Gln	Arg	Cys	Gly	Asn	Gly	Gly	Arg	Ala	Asn	Cys	Asp	Ala	Ser	Leu	
415					420					425					430	
ATC	GTG	ACT	GAG	GAG	CTG	CAC	CTG	ATC	ACC	TTC	GAG	ACT	GAG	GTG	TAC	1406
Ile	Val	Thr	Glu	Glu	Leu	His	Leu	Ile	Thr	Phe	Glu	Thr	Glu	Val	Tyr	
				435					440					445		
CAC	CAA	GGC	CTC	AAG	ATT	GAC	CTA	GAG	ACC	CAC	TCC	TTG	CCA	GTT	GTG	1454
His	Gln	Gly	Leu	Lys	Ile	Asp	Leu	Glu	Thr	His	Ser	Leu	Pro	Val	Val	
			450					455					460			
GTG	ATC	TCC	AAC	ATC	TGT	CAG	ATG	CCA	AAT	GCT	TGG	GCA	TCA	ATC	CTG	1502
Val	Ile	Ser	Asn	Ile	Cys	Gln	Met	Pro	Asn	Ala	Trp	Ala	Ser	Ile	Leu	
		465					470					475				

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TGG Trp 480	TAT Tyr 480	AAC Asn 480	ATG Met 480	CTG Leu 480	ACC Thr 485	AAT Asn 485	AAC Asn 485	CCC Pro 485	AAG Lys 485	AAC Asn 490	GTG Val 490	AAC Asn 490	TTC Phe 490	TTC Phe 490	ACT Thr 490	1550
AAG Lys 495	CCG Pro 495	CCA Pro 495	ATT Ile 495	GGA Gly 500	ACC Thr 500	TGG Trp 500	GAC Asp 500	CAA Gln 505	GTG Val 505	GCC Ala 505	GAG Glu 505	GTG Val 505	CTC Leu 510	AGC Ser 510	TGG Trp 510	1598
CAG Gln 515	TTC Phe 515	TCG Ser 515	TCC Ser 515	ACC Thr 515	ACC Thr 515	AAG Lys 515	CGA Arg 520	GGG Gly 520	CTG Leu 520	AGC Ser 520	ATC Ile 520	GAG Glu 525	CAG Gln 525	CTG Leu 525	ACA Thr 525	1646
ACG Thr 530	CTG Leu 530	GCT Ala 530	GAG Glu 530	AAG Lys 530	CTC Leu 530	CTA Leu 535	GGG Gly 535	CCT Pro 535	GGT Gly 535	GTG Val 535	AAC Asn 540	TAC Tyr 540	TCA Ser 540	GGG Gly 540	TGT Cys 540	1694
CAG Gln 545	ATC Ile 545	ACA Thr 545	TGG Trp 545	GCT Ala 550	AAA Lys 550	TTC Phe 550	TGC Cys 550	AAA Lys 555	GAA Glu 555	AAC Asn 555	ATG Met 555	GCT Ala 555	GGC Gly 555	AAG Lys 555	GGC Gly 555	1742
TTC Phe 560	TCC Ser 560	TTC Phe 560	TGG Trp 560	GTC Val 565	TGG Trp 565	CTA Leu 565	GAC Asp 565	AAT Asn 570	ATC Ile 570	ATC Ile 570	GAC Asp 570	CTT Leu 570	GTG Val 570	AAA Lys 570	AAG Lys 570	1790
TAT Tyr 575	ATC Ile 575	TTG Leu 575	GCC Ala 580	CTT Leu 580	TGG Trp 580	AAT Asn 585	GAA Glu 585	GGG Gly 585	TAC Tyr 585	ATC Ile 585	ATG Met 585	GGT Gly 585	TTC Phe 585	ATC Ile 585	AGC Ser 585	1838
AAG Lys 595	GAG Glu 595	CGG Arg 595	GAG Glu 595	CGG Arg 595	GCC Ala 595	ATC Ile 595	CTA Leu 600	AGC Ser 600	ACA Thr 600	AAG Lys 605	CCC Pro 605	CCG Pro 605	GGC Gly 605	ACC Thr 605	TTC Phe 605	1886
CTA Leu 610	CTG Leu 610	CGC Arg 610	TTC Phe 610	AGC Ser 610	GAG Glu 615	AGC Ser 615	AGC Ser 615	AAA Lys 615	GAA Glu 615	GGA Gly 615	GGG Gly 615	GTC Val 620	ACT Thr 620	TTC Phe 620	ACT Thr 620	1934
TGG Trp 625	GTG Val 625	GAA Glu 625	AAG Lys 625	GAC Asp 630	ATC Ile 630	AGT Ser 630	GGC Gly 630	AAG Lys 635	ACC Thr 635	CAG Gln 635	ATC Ile 635	CAG Gln 635	TCT Ser 635	GTA Val 635	GAG Glu 635	1982
CCA Pro 640	TAC Tyr 640	ACC Thr 640	AAG Lys 645	CAG Gln 645	CAG Gln 645	CTG Leu 645	AAC Asn 645	AAC Asn 650	ATG Met 650	TCA Ser 650	TTT Phe 650	GCT Ala 650	GAA Glu 650	ATC Ile 650	ATC Ile 650	2030
ATG Met 655	GGC Gly 655	TAT Tyr 660	AAG Lys 660	ATC Ile 660	ATG Met 660	GAT Asp 665	GCG Ala 665	ACC Thr 665	AAC Asn 665	ATC Ile 665	CTG Leu 670	GTG Val 670	TCT Ser 670	CCA Pro 670	CTT Leu 670	2078
GTC Val 675	TAC Tyr 675	CTC Leu 675	TAC Tyr 675	CCC Pro 675	GAC Asp 675	ATT Ile 680	CCC Pro 680	AAG Lys 680	GAG Glu 680	GAG Glu 680	GCA Ala 685	TTT Phe 685	GGA Gly 685	AAG Lys 685	TAC Tyr 685	2126
TGT Cys 690	AGG Arg 690	CCC Pro 690	GAG Glu 690	AGC Ser 690	CAG Gln 695	GAG Glu 695	CAC His 695	CCC Pro 695	GAA Glu 695	GCC Ala 700	GAC Asp 700	CCA Pro 700	GGT Gly 700	AGT Ser 700	GCT Ala 700	2174
GCC Ala 705	CCG Pro 705	TAC Tyr 705	CTG Leu 710	AAG Lys 710	ACC Thr 710	AAG Lys 710	TTC Phe 710	ATC Ile 715	TGT Cys 715	GTG Val 715	ACA Thr 715	CCA Pro 715	ACG Thr 715	ACC Thr 715	TGC Cys 715	2222
AGC Ser 720	AAT Asn 720	ACC Thr 720	ATT Ile 725	GAC Asp 725	CTG Leu 725	CCG Pro 725	ATG Met 725	TCC Ser 730	CCC Pro 730	CGC Arg 730	ACT Thr 730	TTA Leu 730	GAT Asp 730	TCA Ser 730	TTG Leu 730	2270
ATG Met 735	CAG Gln 735	TTT Phe 740	GGA Gly 740	AAT Asn 740	AAC Asn 740	GGT Gly 745	GAA Glu 745	GGT Gly 745	GCT Ala 745	GAG Glu 745	CCC Pro 745	TCA Ser 745	GCA Ala 745	GGA Gly 745	GGG Gly 745	2318

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CAG TTT GAG TCG CTC ACG TTT GAC ATG GAT CTG ACC TCG GAG TGT GCT	2366
Gln Phe Glu Ser Leu Thr Phe Asp Met Asp Leu Thr Ser Glu Cys Ala	
755 760 765	
ACC TCC CCC ATG TGAGGAGCTG AAACCAGAAG CTGCAGAGAC GTGACTTGAG	2418
Thr Ser Pro Met	
770	
ACACCTGCCC CGTGCTCCAC CCCTAAGCAG CCGAACCCCA TATCGTCTGA AACTCCTAAC	2478
TTTGTGGTTC CAGATTTTTT TTTTAAATTT CCTACTTCTG CTATCTTTGG GCAATCTGGG	2538
CACTTTTTTAA AAGAGAGAAA TGAGTGAGTG TGGGTGATAA ACTGTTATGT AAAGAGGAGA	2598
GACCTCTGAG TCTGGGGATG GGGCTGAGAG CAGAAGGGAG GCAAAGGGGA ACACCTCCTG	2658
TCCTGCCCCG CTGCCCTCCT TTTTCAGCAG CTCGGGGGTT GGTGTGTTAGA CAAGTGCCTC	2718
CTGGTGCCCA TGGCTACCTG TTGCCCCACT CTGTGAGCTG ATACCCCAT TCTGGGAACTC	2778
CTGGCTCTGC ACTTTCAACC TTGCTAATAT CCACATAGAA GCTAGGACTA AGCCCAGGAG	2838
GTTCTCTTTT AAATTAAAAA AAAAAAAAAA A	2869
(2) INFORMATION FOR SEQ ID NO:12:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 770 amino acids	
(B) TYPE: amino acid	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: protein	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
Met Ala Gln Trp Asn Gln Leu Gln Gln Leu Asp Thr Arg Tyr Leu Lys	
1 5 10 15	
Gln Leu His Gln Leu Tyr Ser Asp Thr Phe Pro Met Glu Leu Arg Gln	
20 25 30	
Phe Leu Ala Pro Trp Ile Glu Ser Gln Asp Trp Ala Tyr Ala Ala Ser	
35 40 45	
Lys Glu Ser His Ala Thr Leu Val Phe His Asn Leu Leu Gly Glu Ile	
50 55 60	
Asp Gln Gln Tyr Ser Arg Phe Leu Gln Glu Ser Asn Val Leu Tyr Gln	
65 70 75 80	
His Asn Leu Arg Arg Ile Lys Gln Phe Leu Gln Ser Arg Tyr Leu Glu	
85 90 95	
Lys Pro Met Glu Ile Ala Arg Ile Val Ala Arg Cys Leu Trp Glu Glu	
100 105 110	
Ser Arg Leu Leu Gln Thr Ala Ala Thr Ala Ala Gln Gln Gly Gly Gln	
115 120 125	
Ala Asn His Pro Thr Ala Ala Val Val Thr Glu Lys Gln Gln Met Leu	
130 135 140	
Glu Gln His Leu Gln Asp Val Arg Lys Arg Val Gln Asp Leu Glu Gln	
145 150 155 160	
Lys Met Lys Val Val Glu Asn Leu Gln Asp Asp Phe Asp Phe Asn Tyr	
165 170 175	

Lys Thr Leu Lys Ser Gln Gly Asp Met Gln Asp Leu Asn Gly Asn Asn
 180 185 190
 Gln Ser Val Thr Arg Gln Lys Met Gln Gln Leu Glu Gln Met Leu Thr
 195 200 205
 Ala Leu Asp Gln Met Arg Arg Ser Ile Val Ser Glu Leu Ala Gly Leu
 210 215 220
 Leu Ser Ala Met Glu Tyr Val Gln Lys Thr Leu Thr Asp Glu Glu Leu
 225 230 235 240
 Ala Asp Trp Lys Arg Arg Pro Glu Ile Ala Cys Ile Gly Gly Pro Pro
 245 250 255
 Asn Ile Cys Leu Asp Arg Leu Glu Asn Trp Ile Thr Ser Leu Ala Glu
 260 265 270
 Ser Gln Leu Gln Thr Arg Gln Gln Ile Lys Lys Leu Glu Glu Leu Gln
 275 280 285
 Gln Lys Val Ser Tyr Lys Gly Asp Pro Ile Val Gln His Arg Pro Met
 290 295 300
 Leu Glu Glu Arg Ile Val Glu Leu Phe Arg Asn Leu Met Lys Ser Ala
 305 310 315 320
 Phe Val Val Glu Arg Gln Pro Cys Met Pro Met His Pro Asp Arg Pro
 325 330 335
 Leu Val Ile Lys Thr Gly Val Gln Phe Thr Thr Lys Val Arg Leu Leu
 340 345 350
 Val Lys Phe Pro Glu Leu Asn Tyr Gln Leu Lys Ile Lys Val Cys Ile
 355 360 365
 Asp Lys Asp Ser Gly Asp Val Ala Ala Leu Arg Gly Ser Arg Lys Phe
 370 375 380
 Asn Ile Leu Gly Thr Asn Thr Lys Val Met Asn Met Glu Glu Ser Asn
 385 390 395 400
 Asn Gly Ser Leu Ser Ala Glu Phe Lys His Leu Thr Leu Arg Glu Gln
 405 410 415
 Arg Cys Gly Asn Gly Gly Arg Ala Asn Cys Asp Ala Ser Leu Ile Val
 420 425 430
 Thr Glu Glu Leu His Leu Ile Thr Phe Glu Thr Glu Val Tyr His Gln
 435 440 445
 Gly Leu Lys Ile Asp Leu Glu Thr His Ser Leu Pro Val Val Val Ile
 450 455 460
 Ser Asn Ile Cys Gln Met Pro Asn Ala Trp Ala Ser Ile Leu Trp Tyr
 465 470 475 480
 Asn Met Leu Thr Asn Asn Pro Lys Asn Val Asn Phe Phe Thr Lys Pro
 485 490 495
 Pro Ile Gly Thr Trp Asp Gln Val Ala Glu Val Leu Ser Trp Gln Phe
 500 505 510
 Ser Ser Thr Thr Lys Arg Gly Leu Ser Ile Glu Gln Leu Thr Thr Leu
 515 520 525
 Ala Glu Lys Leu Leu Gly Pro Gly Val Asn Tyr Ser Gly Cys Gln Ile
 530 535 540

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Thr Trp Ala Lys Phe Cys Lys Glu Asn Met Ala Gly Lys Gly Phe Ser
 545 550 555 560
 Phe Trp Val Trp Leu Asp Asn Ile Ile Asp Leu Val Lys Lys Tyr Ile
 565 570 575
 Leu Ala Leu Trp Asn Glu Gly Tyr Ile Met Gly Phe Ile Ser Lys Glu
 580 585 590
 Arg Glu Arg Ala Ile Leu Ser Thr Lys Pro Pro Gly Thr Phe Leu Leu
 595 600 605
 Arg Phe Ser Glu Ser Ser Lys Glu Gly Gly Val Thr Phe Thr Trp Val
 610 615 620
 Glu Lys Asp Ile Ser Gly Lys Thr Gln Ile Gln Ser Val Glu Pro Tyr
 625 630 635 640
 Thr Lys Gln Gln Leu Asn Asn Met Ser Phe Ala Glu Ile Ile Met Gly
 645 650 655
 Tyr Lys Ile Met Asp Ala Thr Asn Ile Leu Val Ser Pro Leu Val Tyr
 660 665 670
 Leu Tyr Pro Asp Ile Pro Lys Glu Glu Ala Phe Gly Lys Tyr Cys Arg
 675 680 685
 Pro Glu Ser Gln Glu His Pro Glu Ala Asp Pro Gly Ser Ala Ala Pro
 690 695 700
 Tyr Leu Lys Thr Lys Phe Ile Cys Val Thr Pro Thr Thr Cys Ser Asn
 705 710 715 720
 Thr Ile Asp Leu Pro Met Ser Pro Arg Thr Leu Asp Ser Leu Met Gln
 725 730 735
 Phe Gly Asn Asn Gly Glu Gly Ala Glu Pro Ser Ala Gly Gly Gln Phe
 740 745 750
 Glu Ser Leu Thr Phe Asp Met Asp Leu Thr Ser Glu Cys Ala Thr Ser
 755 760 765
 Pro Met
 770

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAYACNGARC CNATGGARAT YATT

24

(2) INFORMATION FOR SEQ ID NO:14:

Variable	Mean	SD	Min	Max
Age	34.5	10.2	18	65
Gender	0.5	0.5	0	1
Marital status	0.6	0.5	0	1
Education	12.5	1.5	9	16
Income	15.2	5.8	5	35
Health status	0.8	0.4	0	1
Stress level	2.5	1.2	1	4
Life satisfaction	3.2	1.5	1	5
Work engagement	4.1	1.8	1	6
Organizational commitment	3.8	1.6	1	5
Job satisfaction	3.5	1.4	1	5
Turnover intention	1.2	0.8	0	3
Organizational citizenship behavior	2.8	1.1	1	4
Employee well-being	3.0	1.3	1	5
Work-life balance	2.5	1.0	1	4
Job design	3.5	1.2	1	5
Supervisor support	3.8	1.5	1	5
Team cohesion	3.2	1.4	1	5
Organizational culture	3.0	1.3	1	5
Leadership style	3.5	1.2	1	5
Employee engagement	3.8	1.5	1	5
Organizational performance	3.5	1.4	1	5
Customer satisfaction	3.2	1.3	1	5
Employee turnover	1.5	0.9	0	3
Organizational innovation	3.0	1.2	1	5
Employee loyalty	3.5	1.4	1	5
Organizational reputation	3.2	1.3	1	5
Employee commitment	3.8	1.5	1	5
Organizational climate	3.0	1.2	1	5
Employee satisfaction	3.5	1.4	1	5
Organizational effectiveness	3.2	1.3	1	5
Employee productivity	3.8	1.5	1	5
Organizational success	3.5	1.4	1	5
Employee well-being	3.0	1.3	1	5
Work-life balance	2.5	1.0	1	4
Job design	3.5	1.2	1	5
Supervisor support	3.8	1.5	1	5
Team cohesion	3.2	1.4	1	5
Organizational culture	3.0	1.3	1	5
Leadership style	3.5	1.2	1	5
Employee engagement	3.8	1.5	1	5
Organizational performance	3.5	1.4	1	5
Customer satisfaction	3.2	1.3	1	5
Employee turnover	1.5	0.9	0	3
Organizational innovation	3.0	1.2	1	5
Employee loyalty	3.5	1.4	1	5
Organizational reputation	3.2	1.3	1	5
Employee commitment	3.8	1.5	1	5
Organizational climate	3.0	1.2	1	5
Employee satisfaction	3.5	1.4	1	5
Organizational effectiveness	3.2	1.3	1	5
Employee productivity	3.8	1.5	1	5
Organizational success	3.5	1.4	1	5

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

21

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: cDNA

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

18

(i) SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

20

(2) INFORMATION FOR SEQ ID NO:17:

[illegible]

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

25

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr Glu Leu Ile
1 5 10 15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

Gly Tyr Ile Lys Thr Glu
1 5

(2) INFORMATION FOR SEO ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Lys Val Asn Leu Gln Glu Arg Arg Lys Tyr Leu Lys His Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Glu Pro Gln Tyr Glu Glu Ile Pro Ile Tyr Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:
(B) CLONE: Src

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Waksman, et al.

(C) JOURNAL: Nature
(D) VOLUME: 358
(F) PAGES: 646-653
(G) DATE: 1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu Ser Glu Arg
1 5 10 15
Leu Leu Leu Asn Pro Glu Asn Pro Arg Gly Thr Phe Leu Val Arg Glu
20 25 30
Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser Asp Phe Phe
35 40 45
Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg Lys Leu
50 55 60
Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Ser Ser Leu
65 70 75 80
Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu Cys His
85 90 95
Arg Leu Thr Asn Val Cys Pro Thr Ser
100 105

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: Abl

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Overduin, et al.
(C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
(D) VOLUME: 89
(F) PAGES: 11673-11677
(G) DATE: 1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Glu Lys His Ser Trp Tyr His Gly Pro Val Ser Arg Asn Ala Ala Glu
1 5 10 15
Tyr Leu Leu Ser Ser Gly Ile Asn Gly Ser Phe Leu Val Arg Glu Ser
20 25 30
Asp Arg Arg Pro Gly Gln Arg Ser Ile Ser Leu Arg Tyr Glu Glu Gly
35 40 45
Arg Val Tyr His Tyr Arg Ile Asn Thr Ala Ser Asp Gly Lys Leu Tyr
50 55 60

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Val Ser Ser Glu Ser Arg Phe Asn Thr Leu Ala Glu Leu Val His His
65 70 75 80
His Ser Thr Val Ala Asp Gly Leu Ile Thr Thr Leu His Tyr Pro Ala
85 90 95
Pro Lys Arg

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Lck

- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Eck, et al.
 - (C) JOURNAL: Nature
 - (D) VOLUME: 362
 - (F) PAGES: 87-91
 - (G) DATE: 1993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Trp Phe Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu
1 5 10 15
Ala Pro Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser
20 25 30
Thr Ala Gly Ser Phe Ser Leu Ser Val Arg Asp Asp Phe Asp Gln Asn
35 40 45
Gln Gly Glu Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly
50 55 60
Gly Phe Tyr Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Asp Leu
65 70 75 80
Val Arg His Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser
85 90 95
Arg Pro Cys Gln Thr Gln
100

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

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Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
18-24	20.5 (2.5)
25-34	29.5 (4.5)
35-44	39.5 (5.5)
45-54	49.5 (6.5)
55-64	59.5 (7.5)
65-74	69.5 (8.5)
75-84	79.5 (9.5)
85-94	89.5 (10.5)
95-104	99.5 (11.5)
105-114	109.5 (12.5)
115-124	119.5 (13.5)
125-134	129.5 (14.5)
135-144	139.5 (15.5)
145-154	149.5 (16.5)
155-164	159.5 (17.5)
165-174	169.5 (18.5)
175-184	179.5 (19.5)
185-194	189.5 (20.5)
195-204	199.5 (21.5)
205-214	209.5 (22.5)
215-224	219.5 (23.5)
225-234	229.5 (24.5)
235-244	239.5 (25.5)
245-254	249.5 (26.5)
255-264	259.5 (27.5)
265-274	269.5 (28.5)
275-284	279.5 (29.5)
285-294	289.5 (30.5)
295-304	299.5 (31.5)
305-314	309.5 (32.5)
315-324	319.5 (33.5)
325-334	329.5 (34.5)
335-344	339.5 (35.5)
345-354	349.5 (36.5)
355-364	359.5 (37.5)
365-374	369.5 (38.5)
375-384	379.5 (39.5)
385-394	389.5 (40.5)
395-404	399.5 (41.5)
405-414	409.5 (42.5)
415-424	419.5 (43.5)
425-434	429.5 (44.5)
435-444	439.5 (45.5)
445-454	449.5 (46.5)
455-464	459.5 (47.5)
465-474	469.5 (48.5)
475-484	479.5 (49.5)
485-494	489.5 (50.5)
495-504	499.5 (51.5)
505-514	509.5 (52.5)
515-524	519.5 (53.5)
525-534	529.5 (54.5)
535-544	539.5 (55.5)
545-554	549.5 (56.5)
555-564	559.5 (57.5)
565-574	569.5 (58.5)
575-584	579.5 (59.5)
585-594	589.5 (60.5)
595-604	599.5 (61.5)
605-614	609.5 (62.5)
615-624	619.5 (63.5)
625-634	629.5 (64.5)
635-644	639.5 (65.5)
645-654	649.5 (66.5)
655-664	659.5 (67.5)
665-674	669.5 (68.5)
675-684	679.5 (69.5)
685-694	689.5 (70.5)
695-704	699.5 (71.5)
705-714	709.5 (72.5)
715-724	719.5 (73.5)
725-734	729.5 (74.5)
735-744	739.5 (75.5)
745-754	749.5 (76.5)
755-764	759.5 (77.5)
765-774	769.5 (78.5)
775-784	779.5 (79.5)
785-794	789.5 (80.5)
795-804	799.5 (81.5)
805-814	809.5 (82.5)
815-824	819.5 (83.5)
825-834	829.5 (84.5)
835-844	839.5 (85.5)
845-854	849.5 (86.5)
855-864	859.5 (87.5)
865-874	869.5 (88.5)
875-884	879.5 (89.5)
885-894	889.5 (90.5)
895-904	899.5 (91.5)
905-914	909.5 (92.5)
915-924	919.5 (93.5)
925-934	929.5 (94.5)
935-944	939.5 (95.5)
945-954	949.5 (96.5)
955-964	959.5 (97.5)
965-974	969.5 (98.5)
975-984	979.5 (99.5)
985-994	989.5 (100.5)
995-1004	999.5 (101.5)
1005-1014	1009.5 (102.5)
1015-1024	1019.5 (103.5)
1025-1034	1029.5 (104.5)
1035-1044	1039.5 (105.5)
1045-1054	1049.5 (106.5)
1055-1064	1059.5 (107.5)
1065-1074	1069.5 (108.5)
1075-1084	1079.5 (109.5)
1085-1094	1089.5 (110.5)
1095-1104	1099.5 (111.5)
1105-1114	1109.5 (112.5)
1115-1124	1119.5 (113.5)
1125-1134	

[illegible]